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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 1, 2004, 09:55:43; Search time 45 Seconds Run on:

(without alignments) 2475.065 Million cell updates/sec

US-09-466-778B-11 Title:

1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353 score: Perfect

Scoring table: Sequence:

1017041 segs, 315518202 residues OLIGO Gapop 60.0 , Gapext 60.0

6 Word size :

Searched:

Total number of hits satisfying chosen parameters:

12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

SPTREMBL 25:*

1: sp_archea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

5: sp_human:*

6: sp_mammal:*

7: sp_mhc:*

sp_organelle:*sp_phage:* 9:

unclassified: * sp_vertebrate:* sp_bacteriap:* sp_plant:*
sp_rodent:*
sp_virus:* rvirus:*

sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		sapien	sapien	pien	homo sapien	pier	pier	pier	pier	rus	Bcul	Q8r4u0 mus musculu	rattus norv
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SUMMARIES					_	•	•	_	~		37	2	46
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Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                     Ohara O., Nagase T., Kikuno R., Okumura K.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1192 AA; 128738 MW; 5966BED4B83BD9C1 CRC64;
                                                                                                                                                                                                                                                                   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                             GO; GO:000540; F:inyaluronic acid binding; IEA.
GO; GO:000540; F:inyaluronic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR000782; BIGH3 FAA1.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR000638; Link.
PFam; PF00469; Pasoiclin; 2.
Pfam; PF00469; Pasoiclin; 2.
Pfam; PF00469; Pasoiclin; 2.
Pfam; PF00469; Rasiclin; 3.
PFINTS; PR00115; EGFLAMMININ.
PRINTS; PR01265; LINKAMODILE.
PCDOM; PD009918; Link; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hyaluronan receptor for endocytosis (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ELJ00112 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.8%; Score 98; DB 4; Le
100.0%; Pred. No. 1.4e-94;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1416 AA.
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SMART; SM0045; FAS1; 3.

SMART; SM00445; LINK; 1.

PROSITE; PS0022; BGF_1; 4.

PROSITE; PS01286; EGF_2; 8.

PROSITE; PS01248; LAMININ TYPE EGF; 2.

EGF-like domain; Laminin EGF-like domain.

NON TER

SEQÜENCE 1192 AA; 128738 MW; 5966BED4883
                                                                                                                                                                                                                                                                                EMBL; AK024503; BAB15793.1;
HSSP; P98066; 1TSG.
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                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                      NCBI_TaxID=9606;
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Local Sim
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Matches
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ID QE
AC QE
DT Q11
DT Q11
DT Q11
DT Q11
CG MG
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QBWWQB
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Q8WWQ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                              MEDLINE=22588541; PubMed=12626425;
Zhou B., McGary C.T., Weigel J.A., Saxena A., Weigel P.H.;
"Purification and molecular identification of the human hyaluronan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Spleen;
Jakuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
spleen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 kDa hyaluronan receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.8%; Score 98; DB 4; Length 1416; 100.0%; Pred. No. 1.6e-94; Live 0; Mismatches 0; Indels
                                                                                                                Fereptor for endocytosis.";

I receptor for endocytosis.";

Glycobiology 13:339-349(2003).

R RMBL, AV227444; AA039681.1;

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005198; F:calcium ion binding; IEA.

R GO; GO:0005198; F:calcium ion binding; IEA.

GO; GO:0005198; F:calcium ion binding; IEA.

R GO; GO:0005198; F:calcium ion binding; IEA.

R InterPro; IPR006198; EGF [ike.

R InterPro; IPR00629; EGF; B.

R InterPro; IPR00649; Link.

R InterPro; IPR00659; Inink.

R Fam; PR00608; EGF; B.

R Fam; PR00608; EGF; B.

R Fam; PR00191; EGF; B.

R Fam; PR00191; EGF; B.

R SWART; SW00179; EGF; B.

R SWART; SW00179; EGF; II.

R SWART; SW00179; EGF; II.

R SWART; SW00179; EGF; II.

R ROSITE; PS01186; EGF; 2.

R ROSITE; PS01186; EGF; 2.

R ROSITE; PS01186; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocytosis.
1416 AA; 154089 MW; 85A216D38E3B10DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1236 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 1273
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
FLJ00122 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 1...
Marches 98; Conservative 0; Mismatches
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<1 1416
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  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
NON TER
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OOTEST
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1496 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P., Obchanson S., Birk R., Hakiy N., Franke P., Kodelja V., Kannicht C., Orfanos C.E., Johannson S., Goordt S., "Stabilin-1 and stabilin-2 constitute a novel family of fasciclin domain-constaining adhesion molecules associated with endothelial-submitted (JUL-2000) to the EMBL/Genbank/DDBJ databases."; EMBL, AL29565; CACCR2105.1; EMBL/Genbank/DDBJ databases. BMBL, ACS9565; CACCR2105.1; GO, GO:0005540; F: Myaluronic acid binding; IEA.

GO; GO:0005198; F: Etructural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bureleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 27.8%; Score 98; DB 4; Length 1736; l Similarity 100.0%; Pred. No. 1.9e-94; 98; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER 1
SEQÜENCE 1736 AA; 187887 MW; 50982047E43925F2 CRC64;
           to the EMBL/GenBank/DDBJ databases.
1556 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
612bilin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000783, BIGHS FASI.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000538; Link.
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Pfam, PF02469, Fasciclin, 5.
Pfam, PF00193, Xlink, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22206516; PubMed=12077138;
Adachi H., Tsujimoto M.;
"TERL-1. a novel scavenger receptor with in vitro bacteria-binding and
                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        Length 2551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD00018; Link; 1.

SMART; SM0018; EGF; 20.

SMART; SM0018; EGF; 20.

SMART; SM00454; FAS1; 7.

PROSITE; PS00126; EGF 1; 7.

PROSITE; PS01186; EGF 2; 16.

PROSITE; PS0213; FAS1; 7.

PROSITE; PS02186; LAMININ TYPE EGF; 2.

EGF-like domain; Laminin EGF-like domain.

SEQUENCE 2551 AA; 276992 MW; 60A44651CCC2BE69 CRC64;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             2371 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 2408
                                                                                                                                                                                                                                                                                                                                                                                                                     229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                    27.8%; Score 98; DB 4; Le
100.0%; Pred. No. 2.8e-94;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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InterPro; IPR001881; BGF Ca.
InterPro; IPR0062109; BGF like.
InterPro; IPR0062109; Laminin_BGF.
InterPro; IPR0002049; Laminin_BGF.
InterPro; IPR0002049; Laminin_BGF.
InterPro; IPR000238; Link.
InterPro; IPR000737; Squash.
Pfam; PF00008; EGF; 16.
Pfam; PF00108; Xiink; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom, PD000918; Link; 1.
SMART; SM00181, EGF 72.
SMART; SM00179; EGF CA; 8.
SMART; SM00180; EGF Lam; 5.
SMART; SM00284; FAS1; 7.
SMART; SM00284; FAS1; 7.
PROSITE; PS00022; EGF 1; 7.
PROSITE; PS01186; EGF 2; 16.
PROSITE; PS01186; EGF 2; 16.
PRINTS; PRODOLL; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Db
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                                                                                                                                                                                                169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 228
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SEQUENCE FROM N.A.
Tao Q., Zhang W., Cao X.,
"Molecular cloning and characterization of human FELL sharing homology with CD44 ".
With CD44 ".
Submitted (JUV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF166476; AAF82398.1; --
HSSP; P98066; ITSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park S.-Y., Kim I.-S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY311388; AAP74558.1; -..
SEQUENCE 2551 AA; 276986 MW; 3ACB6A6C3CB80044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                               0
                                                                                 27.8%; Score 98; DB 4; Length 2551; 100.0%; Pred. No. 2.8e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2551;
                                                                                                                                         0; Indels
PROSITE; PS01248; LAMININ TYPE EGF; 2. SEQUENCE 2551 AA; 277026 MW; 3ADDF3F5BD2019C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                          2371 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 2408
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                                                                                                                                                                                                                                                                                                             229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO: GO:0005540; F:Byaluronic acid binding; IEA.
GO: GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last annotation update)
CD44-like precursor FBLL.
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100.0%; Pred. No. 2.8e-94;
tive 0; Mismatches 0;
                                                                                                            100.0%; Pred. No. 2.80
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 2551 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                         Best Local Similarity 100. Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=9606;
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PROSITE; PS50213; FAS1; 3.
PROSITE; PS01248; LAMININ TYPE EGF; 1.
Hypothetical protein; EGF-like domain; Laminin EGF-like domain.
NON_TER
                                                                                         ch 26.3%; Score 93; DB 4; Length 1069; I Similarity 100.0%; Pred. No. 2.5e-89; 93; Conservative 0; Mismatches 0; Indels
                                                             SEQUENCE 1069 AA; 115666 MW; 0480960932164D63 CRC64;
                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
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                                                                                            Query Match
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NON TER
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                                                                                                                   Matches
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                                                                                                        Best
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                                                                                                                                                                                                                                                                                                                       1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL, Ali33021; CAB61358.1; -.
                                                                                                                                                                                                                                                                          Length 897;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                           897 AA; 97585 MW; EB920AF36101E388 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005540; F:hyaluronic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR000782; BIGH3 FAS1.
R InterPro; IPR000509; BGF Ire.
R InterPro; IPR0005049; IEGF.
R InterPro; IPR0005049; Liminin_EGF.
R InterPro; IPR000538; Link.
R Pfam; PF02469; PSeciclin; 2.
R Pfam; PF02469; PSeciclin; 2.
R Pfam; PF02469; RSeciclin; 2.
R Pfam; PF02469; RSeciclin; 2.
R Pfam; PF02469; LinkAndoubus.
R PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UF98;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
DKF2P434E0321.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                   26.3%; Score 93; DB 4; Le
100.0%; Pred. No. 2.2e-89;
                                                                                                                                                                                                                                                                                                                                                                                          61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 4.12.
Marches 93; Conservative 0; Mismatches
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InterPro; IPR000782; BIGH3 FASI.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006538; Laminin_EGF.
Pfam; PF001008; EGF; 4.
Pfam; PF00193; Xlink; 1.
PRINTS; PR01265; LINKODULE.
ProDom; PD000918; Link; 1.
PROSIT; SM00181; EGF; 5.
SMART; SM00545; LINK; 1.
PROSITE; PS01022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 4.
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SMART; SM00181; EGF, 8.
SMART; SM0045; LINK, 1.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF_2; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                   1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTYGVFHL 60
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TISSUB-Liver;
Ulbrich S.E., Thoene S.;
"Expression of the hyaluronan system in the bovine oviduct.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 500;
                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative hyaluronan receptor for endocytosis (Fragment).
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ550060; CAD79334.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 AA; 54479 MW; C93AA6404B103582 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Similar to CD44-like precursor FELL (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.1%; Score 32; DB 6; Le
Sest Local Similarity 100.0%; Pred. No. 8.2e-25;
Atches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                             61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 LHFQDTTVGVFHLRSPLGQYKLTFDKAREACA 453
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QBCFM6;
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Q8CFM6
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A The FANTOM CONSOrtium,
The FIREN Genome Exploration Research Group Phase I & II Team;
The FANTOM CONSOrtium,
The FANTOM CONSOrtium,
The FIREN Genome Exploration Research Group Phase I & II Team;
The FIREN Genome Exploration Research Group Phase I & II Team;
The FIREN Genome Exploration Research Group Phase I & II Team;
The FIREN Genome Exploration Genome Passed on functional annotation of Go, 700 full-length cDNAs.";
The FEBL; ARO1452; BAC28741.;
The GO; GO:0005159; Fistructural molecule activity; IEA.
DR GO; GO:000155; P:cell adhesion; IEA.
DR GO; GO:000159; P:cell adhesion; IEA.
DR GO; GO:000159; P:Cell adhesion; IEA.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR00638; Link; 1.
DR PFam; PF00189; EGF; 3.
DR Pfam; PF00189; EGF; 1.
DR PROMET; SM00180; EGF; 1.
DR SWART; SM00180; EGF Lam; 2.
DR SWART; SM00180; EGF Lam; 2.
DR ROSITE; PS01186; EGF 2; 4.
DR PROSITE; PS01186; EGF 2; 4.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=BALB/c; TISSUS=Liver;

X MEDLINE=21818465; PubMed=11829752;

A Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P., A. Johansson S., Svineng G., Framche P., Kannicht C., Kzhyshkowska J., A. Longati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Velten F.W., Johannson S., Goerdt S.;

R Jongati P., Grant Johannson S., Goerdt S.;

R Jongati P., Grant Dinding; IEA.

DR GO; GO:0005198; F.sctin binding; IEA.

BR GO; GO:0005198; F.sctin chural molecule activity; IEA.

GO; GO:0007155; P:cell adhesion; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR001599; Actbind_actnin.

DR InterPro; IPR006209; EGF_11ke.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
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8.5%; Score 30; DB 11; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              894 AA; 97059 MW; 3286E2A223CFBB96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-07N-2002 (TrEMBLrel. 21, Created)
01-07N-2002 (TrEMBLrel. 21, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2559 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  530 CVDLHFQDTTVGVFHLRSPLGQYKLTFDKA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 CVDLHFQDTTVGVFHLRSPLGQYKLTFDKA 74
STRAIN=C57BL/6J; TISSUE=Diencephalon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stabilin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;

MEDLINE=22169209; PubMed=12181351;

Anou B., Weigel J.A., Saxena A., Weigel P.H.;

Anolecular Cloning and Functional Expression of the Rat 175-kDa

"Molecular Cloning and Functional Expression of the Rat 175-kDa

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hyaluronan receptor (A for endocytosis HARE precursor (Fragment)
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.5%; Score 30; DB 11; Length 2559; Best Local Similarity 100.0%; Pred. No. 5e-22; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2559 AA; 277530 MW; 1C9855AD61EFF015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2195 CVDLHFQDTTVGVFHLRSPLGQYKLTFDKA 2224
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                    InterPro; IPR00249; Laminin_BGF.
InterPro; IPR002049; Laminin_BGF.
InterPro; IPR002049; Laminin_BGF.
InterPro; IPR002049; Link.
Pfam; PF00469; Fasciclin; 6.
Pfam; PF00193; Xlink; 1.
PR1075; PR00011; BGFLAMININ.
ProDom; PD000918; Link; 1.
SWART; SW00548; PAS1; 7.
SWART; SW00445; Link; 1.
PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS01022; BGF 1; 7.
PROSITE; PS01186; EGF 2; 16.
PROSITE; PS01248; LAMININ_TYPE_BGF; 2.
BGF-like domain.
SEQUENCE 2559 AA; 277530 WW; 1C985SAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00181; EGF; 11.
SMART; SM0179; EGF CA; 2.
SMART; SM00179; EGF CA; 2.
SMART; SM00445; Link; 1.
PROSITE; PS01025; EGF 1; 3.
PROSITE; PS01018; EGF 1; 3.
PROSITE; PS0118; EGS1; 4.
PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01265; LINKMODULE. ProDom; PD000918; Link; 1.
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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o O

Receptor. NON TER 1 SEQUENCE 1431 AA; 155914 MW; 3340A8F7AF366722 CRC64;

Query Match 7.1%; Score 25; DB 11; Length 1431; Best Local Similarity 100.0%; Pred. No. 5.9e-17; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps

δ

0;

Search completed: April 1, 2004, 09:58:24 Job time : 46 secs g

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 1, 2004, 09:55:43; Search time 17 Seconds (without alignments) 1081.221 Million cell updates/sec Run on:

Title: Perfect score:

US-09-466-778B-11

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters: O Word size :

0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB ID Result

Description

No matches found

Search completed: April 1, 2004, 09:57:25 Job time: 17 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 1, 2004, 09:55:43; Search time 20 Seconds (without alignments) 1697.780 Million cell updates/sec Run on:

US-09-466-778B-11

Title: Perfect score:

Sequence:

OLIGO

Scoring table:

283366 segs, 96191526 residues Searched:

Gapop 60.0 , Gapext 60.0

6 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	681 hypothetical prote
	ID	1.5
	DB	2
	Length	1069
Query	Match	26.3
	No. Score Match Length DB ID	1 93 26.3 1069 2 7
Result	No.	1 7

ALIGNMENTS

hypothetical protein DKFZp434E0321.1 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T42681
S;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, November 1999
A;Reference number: 222233

A Accession: T42681 A/Status: preliminary A:Molecule type: mRNA A/Residues: 1-870,871-1069 <AAA> A/Cross-references: EMBL.AL133021

A, Experimental source: adult testis; clone DKFZp434E0321
A,Note: the cDNA sequence contains a +1 frameshift near codon 870
C,Genetics:
A,Note: DKFZp434E0321.1

ò Gaps 0; Query Match 26.3%; Score 93; DB 2; Length 1069; Best Local Similarity 100.0%; Pred. No. 6.6e-88; Matches 93; Conservative 0; Mismatches 0; Indels

697 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 756 1 MIGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60 93 61 RSPLGOYKLTFDKAREACANEAATMATYNQLSY g ò

completed: April 1, 2004, 09:58:56 ne : 20 secs Search co

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2, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, A Sequence 20, Sequence 211, Sequence 41, Sequence 41, Sequence 39, Sequence 4, A Sequence 2, A
                                                                                              April 1, 2004, 09:58:28 ; Search time 45 Seconds (without alignments) 2057.758 Million cell updates/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printe and is derived by analysis of the total score distribution.
                                                                                                                                                                                         353
1 MTGPGKHKCECKSHYVGDGL.....ALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40,
Sequence 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT MRW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                    23
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 US-10-028-24BA-40
1 US-09-842-930A-25
1 US-09-842-930A-25
2 US-10-133-172-4
4 US-10-133-172-20
5 US-10-028-24BA-211
5 US-10-107-782-211
5 US-10-107-782-211
5 US-10-107-782-211
6 US-10-107-782-211
7 US-10-107-782-39
1 US-10-107-782-39
1 US-10-028-24BA-4
1 US-10-107-782-4
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                               1069545 segs, 262320428 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Listing first 500 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                            Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                       US-09-466-778B-11
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Match Length DB
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1394
1416
1653
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                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                             Searched:
                                                                                                   Run on:
                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
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Sequence 5, Appli equence 2, Appli Sequence 2, Appli Sequence 82, Appl Sequence 17, Appl equence 55, Appl equence 43, Appl		Polypeptides and 1	Gaps 0;
o ao		and	5; Length 1192; -89; Indels 0;
US-10-133-172-5 US-09-842-930A-2 US-10-133-172-2 US-10-133-172-17 US-09-842-930A-55 US-09-842-930A-53 US-10-133-172-18	ALIGNMENTS	<u>6</u> 70 .	Score 98; DB 15; Pred. No. 1.8e-89; 0; Mismatches 0;
93 14 1431 9 1431 14 106 14 18 14 15 9 1 13 9 1		12-18A-40 12-18A-40 12-18-40 12-18-40 13-18-18-18-18-18-18-18-18-18-18-18-18-18-	27.8%; 100.0%; vative C
15.3 7.11 7.11 7.11 8 8 5.1 8 3 3 7 7 1 8 8 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1		8-248A-40 ce 40, Application US/1 ation No. US20030235882 LINFORMATION: CANT: Shinkets, Richard CANT: Vernet, Corine CANT: Casman, Stacie CANT: Shores, Corine CANT: Shores, Cannes, CANT: Shores, Kimberly CANT: Shores, Raym CANT: Li,	·d 3
16 17 18 18 25 19 20 21 21 15 22 13 13		RESULT I US-10-028-248A-40 Sequence 40, Ap Publication No. GENERAL INFORMAR APPLICANT: Shi APPLICANT: Ca APPLICANT: Ca APPLICANT: Sp APPLICANT: Sp APPLICANT: Sp APPLICANT: Sp APPLICANT: Sc APPLICANT	Query Match Best Local Sim Matches 98;
			, e
	s/sec	ed, () Appl Appl Appl () App	App Appl Appl

Methods

169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 228

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APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REFERENCE: 5864.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT FILING DATE: 2002-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 09/286,468
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1176 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 228
                                                                                                                                                                                                                                                APPLICANT: Weigel, Paul
TITLE OF INVENTION: Identification of Hyaluronan Receptor for Enddcytosis
FILE REFERENCE: 5820.603
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR PLING DATE: 2000-011-02
PRIOR FILING DATE: 2000-011-02
PRIOR PLING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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1 Similarity 100.0%; Pred. No. 2.1e-89; 
98; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
     1012 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1236 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 27.8%; Score 98; DB 9; L. Similarity 100.0%; Pred. No. 2.1e-89; 98; Conservative 0; Mismatches 0;
                                                                                                                                        US-09-842-930A-25; Sequence 25, Application US/09842930A; Publication No. US20020197681A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/10133172; Publication No. US20030104987A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 25
LENGTH: 1394
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-133-172-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-842-930A-25
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LENGTH: 1416
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US-10-133-172-4
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
952 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1011
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                                                                                       1012 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 1049
                                                       229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
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Best Local Similarity 100.0%; Pred. No. 1.8e-89;
Matches 98; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/266,619
PRIOR APPLICATION NUMBER: 60/26,959
PRIOR FILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
PRIOR PILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR PLING DATE: 2001-04-20
PRIOR PRILING DATE: 2001-04-20
PRIOR PLING DATE: 2001-06-09
PRIOR PRILING DATE: 2001-08-09
PRIOR PRILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
PRIOR PRILING DATE: 2001-03-28
NUMBER: CALCASCELLIST VERSION 0.1
                                                                                                                                                                                                                                             Sequence 40, Application US/10107782
Publication No. US20040018970A1
GENERAL INFORMATION:
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Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Colman, Steve,
Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
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Rothenberg, Mark,
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US-10-107-782-40
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APPLICANT: Rothenberg, Marian
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/25619
PRIOR FILING DATE: 2000-12-19
PRIOR PILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272408
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR PRIOR DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308039
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SEQ ID NO 41
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Kekuda, Ramesh
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Vernet, Corine
Casman, Stacie
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Shenoy, Suresh
Spytek, Kimberly
Gangolli, Esha
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Boldog, Ferenc
Li, Li
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Liu, Xiaohong
Colman, Steven
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Edinger, Shlomit
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Millet, Isabelle
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                                                                                                                                                                                                                                                                                                          LENGTH: 897
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 93; Conserv
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APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
                                                                                                                                                  APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FLIE REFERENCE: 5864.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 09/842,930
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%; Score 98; DB 14; Length 1653; 100.0%; Pred. No. 2.4e-89; cive 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/256619
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                                                            IS-10-133-172-20
Sequence 20, Application US/10133172
Publication No. US20030104987A1
GENERAL INFORMATION:
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Zerhusen, Bryan
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Tchernev, Velizar
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Edinger, Shlomit
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Millet, Isabelle
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Miller, Charles
Boldog, Ferenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spytek,
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LENGTH: 1653
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APPLICANT:
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILLE REFERENCE: 21402-22CIP
CURRENT APPLICATION NUMBER: 105/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR PRILICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/265,619
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-07-26
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                                                                                                                                                                                                                                                                        Query Match 26.3%; Score 93; DB 15; Length 897; Best Local Similarity 100.0%; Pred. No. 1.5e-84; Matches 93; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
           PRIOR APPLICATION NUMBER: 60/279,344
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CURASEQLIST VERSION 0.1
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Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Edinger, Shlomit,
APPLICANT: Gangolli, Esha,
APPLICANT: Kekuda, Ramesh,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
Patturajan, Meera,
Rothenberg, Mark,
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Vernet, Corine,
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                                                                                                                  SEQ ID NO 41
LENGTH: 897
                                                                                                                                                                    TYPE: PRT
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APPLICANT
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APPLICANT: Vernet, Corine,
APPLICANT: Zerthusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REPERENCE: 21402-222CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT APPLICATION DAIE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 MTGPGKHKCECKSHYVGDGLNCEPPQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 548
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                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                      Length 897;
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Best Local Similarity 100.0%; Pred. No. 1.5e-84;
Matches 93; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/266,619
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR APPLICATION NUMBER: 60/202,969
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272,408
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308039
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SEQ ID NO 211
LENGTH: 897
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PRIOR APPLICATION NUMBER: 60/308,039
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 41, Application US/10107782; Publication No. US20040018970A1; GENERAL INFORMATION:
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Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Rothenberg, Mark,
Sciore, Paul,
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Gangolli, Esha,
Kekuda, Ramesh,
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
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US-10-028-248A-211
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APPLICANT:
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
                                                                                                                                                                      1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                            Length 1069;
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                                                                                         0; Indels
                                       ch 26.3%; Score 93; DB 15; I
| Similarity 100.0%; Pred. No. 1.8e-84;
93; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    757 RSPLGQYKLTFDKAREACANBAATMATYNQLSY 789
                                                                                                                                                                                                                                          61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
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CURRENT FILING DATE: 2002-03-27
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PRIOR APPLICATION NUMBER: 10/028,248
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2001-02-8
PRIOR PILING DATE: 2001-01-9
PRIOR PILING DATE: 2001-02-8
PRIOR APPLICATION NUMBER: 60/272,408
PRIOR APPLICATION NUMBER: 60/272,408
PRIOR PILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/10107782 Publication No. US20040018970A1 GENERAL INFORMATION:
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SEQ ID NO 39
LENGTH: 1069
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Sl, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Colman, Steve,
Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Shenoy, Suresh,
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Vernet, Corine,
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ORGANISM: Homo sapiens
                                       Query Match
Best Local Similarity
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Best Local Similarity
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US-10-107-782-39
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APPLICANT: Millet, Isabelle
APPLICANT: Millet, Mark
APPLICANT: Rothenberg, Mark
ITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
ITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                      489 MTGPGRGHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 548
                                                                                                                                                                                                                                                                                    1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                        Length 897;
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                     Score 93; DB 15; I Pred. No. 1.5e-84;
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                                                                                                                                                                                                                                                                                                                                                                                      61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 93; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: 60/272408
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-06-09
PRIOR PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
SOFTWARE: PAGNIN VINGER: 60/311266
PRIOR FILING DATE: 201-08-09
SOFTWARE: PAGNIN VINGER: 60/311266
PRIOR PILING DATE: 201-08-09
SOFTWARE: PAGNIN VINGER: 60/311266
PRIOR PILING DATE: 201-08-09
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PRIOR APPLICATION NUMBER: 60/256619
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PRIOR APPLICATION NUMBER: 60/262959
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Taupier Jr, Raymond J
Kekuda, Ramesh
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 211
LENGTH: 897
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
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Edinger, Shlomit
Stone, David
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Miller, Charles
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; ORGANISM: Homo sapiens
US-10-028-248A-39
                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-211
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REPERENCE: 21402-22221
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028,248
                                2250 MIGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 2309
  1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
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NAME/KEY: misc feature
LOCATION: (371)...(371)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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                                                                                         61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
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PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PRING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/285,189
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CHASSEQLIST VERSION 0.1
                                                                                                                                                                                                                                        Sequence 4, Application US/10107782
Publication No. US20040018970A1
GENERAL INFORMATION:
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Tchernev, Velizar,
Vernet, Corine,
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Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Bdinger, Shlomit,
APPLICANT: Gangolli, Esha,
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Rothenberg, Mark,
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Malyankar, Uriel,
Miller, Charles,
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ORGANISM: Homo sapiens
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US-10-107-782-4
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IIILE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
IIILE OF INVENTION: Thereof
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                                                                       1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
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  0; Gaps
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NAME/SKY. UNSURE
LOCATION: (371)..(372)
OTHER INFORMATION: Wherein Xaa is any naturally occurring amino acid
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  Indels
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                                                                                                                                                              61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
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CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-02-29
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-06-09
PRIOR PILING DATE: 2001-06-09
PRIOR PILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SEQ ID NO 4
LENGER PATCHTIN VET: 2.1
  0; Mismatches
                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10028248A Publication No. US20030235882A1 GENERAL INFORMATION:
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Vernet, Corine
Casman, Stacie
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APPLICANT: Patturajan, Meera
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Shenoy, Suresh
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Millet, Isabelle
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Edinger, Shlomit
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  93; Conservative
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APPLICANT: Sciore, Paul
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: No. US20030215882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/26599
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/285189
PRIOR PLING DATE: 2001-04-20
PRIOR PLING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
NUMBER OF SEQ ID NOS: 21
                                                                                                                    2250 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 2309
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                                              0; Gaps
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LOCATION: (55)..(56)
OTHER INFORMATION: Wherein Xaa is any naturally occurring amino acid
    Length 2420;
                                         0; Indels
Query Match 26.3%; Score 93; DB 15; L
Best Local Similarity 100.0%; Pred. No. 3.8e-84;
Matches 93; Conservative 0; Mismatches 0;
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                                                                                                                                                                              61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
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APPLICANT: Shimkets, Richard APPLICANT: Patturajan, Meera
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Vernet, Corine
Casman, Stacie
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Smithson, Glennda
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Tchernev, Velizar
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Shenoy, Suresh
Spytek, Kimberly
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Bdinger, Shlomit
Stone, David
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SEQ ID NO 2
LBNGTH: 2675
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US-10-028-248A-2
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APPLICANT:
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-2222CH
FULE REFERENCE: 21402-222CH
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                        2303 MIGPGKHKCECKSHYVGDGINCEPEQDPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 2362
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                                                                                                                        Gaps
; OTHER INFORMATION: Wherein Xaa is any naturally occurring amino acid US-10-028-248A-2
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                                                                     Ouery Match 26.3%; Score 93; DB 15; Length 2675; Best Local Similarity 100.0%; Pred. No. 4.1e-84; Matches 93; Conservative 0; Mismatches 0; Indels 0
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR PAPLICATION NUMBER: 60/22,959
PRIOR PILING DATE: 2000-12-19
PRIOR PELING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/205,189
PRIOR PILING DATE: 2001-04-26
PRIOR PILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-08-09
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 2
LENGTH: 2675
TYPE: PRT
ORGANIEM: Homo sapiens
FEATURE:
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Tchernev, Velizar,
Vernet, Corine,
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Rothenberg, Mark,
Sciore, Paul,
Shenoy, Suresh,
Shimkets, Richard,
Si, Jingsheng,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Spytek, Kimberly,
Stone, David,
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Gangolli, Esha,
Kekuda, Ramesh,
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
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US-10-107-782-2
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APPLICANT:
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APPLICANT:
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APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REPERRANCE: 5864.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT FILING DATE: 2002-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTE: 2001-04-25
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Publication No. US202020197681A1
GENERAL INFORMATION:
APPLICANT: Weigel, Paul
ITIE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
FILE REPERENCE: 5820.603
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (427)...(427)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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LOCATION: (428)...(428)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
LOCATION: (55)...(55)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
                                                                                                                                 LOCATION: (56)...(56)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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; Sequence 5, Application US/10133172
; Publication No. US20030104987A1
; GENERAL INFORMATION:
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                                                                                                         NAME/KEY: misc_feature
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Best Local Similarity
Matches 54; Conserv
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APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REPERENCE: 5864.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/842,930
PRIOR RILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                    7.1%; Score 25; DB 9; Length 1431;
.00.0%; Pred. No. 7.6e-16;
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TITLE OF INVENTION: 29 Human Cancer Associated Proteins
FILE REPERBNCE: PA004P1
CURRENT APLICATION NUMBER: US/10/023,896
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                              Query Match 7.1%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 7.6 Matches 25; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION WINBER: PCT/US00/23794
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-00-06
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 82
LENGTH: 106
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PRIOR APPLICATION NUMBER: 60/199,538 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 56 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 82, Application US/10023896; Publication No. US20030027776A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/10133172; Publication No. US20030104987A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-12-2
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                                                                                                      SEQ ID NO 2
LENGTH: 1431
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US-10-023-896-82
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1 RSPLGQYKLTFDKAR 15

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SEQ ID NO 18
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APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REFERENCE: 5864.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT APPLICATION NUMBER: 60/24.25
RRIOR APPLICATION NUMBER: 60/286,468
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
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APPLICANT: Weigel, Paul
TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
FILE REPERBNUE: 5820.603
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
                                                                                                                                           Gaps
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                                                                                       Query Match 5.7%; Score 20; DB 14; Length 106; Best Local Similarity 100.0%; Pred. No. 7.8e-12; Matches 20; Conservative 0; Mismatches 0; Indels
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4.2%; Score 15; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17, Application US/10133172; Publication No. US20030104987A1; GENERAL INFORMATION:
                                                                                                                                                                                    326 IILVTGAVALAAYSYFRINR 345
                                                                                                                                                                                                               23 IILVTGAVALAAYSYFRINR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TGPGKHKCECKSHYVGDG 19
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SEQ ID NO 17
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-133-172-17
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-842-930A-55
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                          ; ORGANISM: HON
US-10-023-896-82
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LENGTH: 15
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RESULT 23

US-10-133-172-18

US-10-133-172-18

US-10-133-172-18

Sequence 18, Application US/10133172

Publication No. US20030104987A1

GENERAL INFORMATION:

APPLICANT: WEIGEL, DANET A

TILLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS

FILE REFERENCE: 5864.014

CURRENT FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 06/286,468

PRIOR PILING DATE: 2001-04-25

PRIOR FILING DATE: 2001-04-25

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 20

SOFTWARE PATENTING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 20

SOFTWARE PATENTING DATE: 2001-04-25
US-09-842-930A-43

| Sequence 43, Application US/09842930A |
| Publication No. 220020197681A1 |
| GENERAL INFORMATION: Indentification of Hyaluronan Receptor for Endocytosis |
| TITLE OF INVERTION: Indentification of Hyaluronan Receptor for Endocytosis |
| TITLE OF INVERTION: UNMERR: US/09/842,930A |
| TURENT APPLICATION NUMBER: US/09/842,930A |
| FILE REFERENCE: 2000-11-02 |
| PRIOR FILING DATE: 2000-11-02 |
| PRIOR FILING DATE: 2000-04-25 |
| NUMBER OF SEQ ID NOS: 56 |
| NUMBER OF SEQ ID NOS: 56 |
| SOFTWARE: PatentIn version 3.1
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Matches 13; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 13
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

OM protein - protein search, using sw model

April 1, 2004, 09:55:43 ; Search time 22 Seconds (without alignments) 828.362 Million cell updates/sec

353 1 MTGPGKHKCECKSHYVGDGL.....ALAAYSYFRINRKTIGFXHF 353 US-09-466-778B-11

Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

389414 Begs, 51625971 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

Issued Patents AA:*
1: /cgT2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgT2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgT2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgT2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgT2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgT2_6/prodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID Query Score Match Length DB

Description

No matches found

Search completed: April 1, 2004, 09:59:31 Job time: 22 secs

RESULT 1

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein 1, 2004, 09:55:42 ; Search time 58 Seconds
(without alignments)
1719.643 Million cell updates/sec April Run on:

ritle:

US-09-466-778B-11 Perfect score:

353 1 MTGPGKHKCECKSHYVGDGL.....ALAAVSYFRINRKTIGFXHF 353 OFIGO Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

Gapop 60.0 , Gapext 60.0

ō, Word size : Total number of hits satisfying chosen parameters:

20

seq length: 0
seq length: 200000000 Minimum DB Maximum DB

Post-processing: Listing first 500 summaries

Database

geneseqp2003as:*geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp2001a:* geneseqp2002a:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aay93913 A human h				Aab83359 NOV3 prot	Aab83364 NOV8 prot	Aab83362 NOV6 prot	Abj10588 Human nov		Abj10586 Human nov		Aab83358 NOV2 prot	Abg72500 Human 190	Aam47675 Rat Hyalu	Abg72498 Rat 175kD	Aau00893 Human can	Abq72512 Human 190	Human	Human	
	E1	AAY93913	AAM47684	ABG72499	ABG72514	AAB83359	AAB83364	AAB83362	ABJ10588	ABJ10587	ABJ10586	AAB42164	AAB83358	ABG72500	AAM47675	ABG72498	AAU00893	ABG72512	AAM47702	AAM47690	ABG72513
	DB	3	Ŋ	9	ø	4	4	4	Ŋ	'n	Ŋ	m	4	9	S	φ	4	9	2	Ŋ	9
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%	Query Match	97.7	27.8	27.8	27.8	26.3	26.3	26.3	26.3	26.3	26.3	24.1	16.1	15.3	7.1	7.1	5.7	5.1	4.2	3.7	3.7
	Score	345	86	96	86	93	93	93	93	93	93	85	57	54	25	25	20	18	15	13	13
	Result No.		7	m	4	Ŋ	9	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20

OE-

Claim 11; Fig 4A-B; 457pp; English.

Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP; proliferative condition; metastasis; inflammation; ischemia; bost defence dysfunction; immune surveillance dysfunction; arthritis; multiple sclerosis; autoimmunity; immune dysfunction; allergy. New hyaluron-binding proteins, known as full-length WF-HABP, WF-HABP, HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis. encoded by GNA" 'note= "unspecified amino acid encoded by TNT" "unspecified amino acid encoded by CAN" 'note= "unspecified amino acid encoded by TNC" 'note= "unspecified amino acid encoded by NCC" 'note= "unspecified amino acid encoded by YCT" 'note= "unspecified amino acid encoded by NNC' "unspecified amino acid encoded by designated BM-HABP. 'note= "unspecified amino acid 121. .215 /note= "HA binding domain" A human hyaluronan-binding protein, Location/Qualifiers Æ. <u>ы</u> AAY93913 standard; protein; 353 Tsifrina (HUMA-) HUMAN GENOME SCI INC. (AMNA-) AMERICAN NAT RED CROSS. 99WO-US030462. (first entry) 'note= /note= Liau G, WPI; 2000-452376/39. Misc-difference 324 Misc-difference 325 Misc-difference 351 N-PSDB; AAA57365. Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference WO200039166-A1 Homo sapiens. 20-DEC-1999; Hastings GA, 03-OCT-2000 23-DEC-1998; 06-JUL-2000 AAY93913; Domain AAY93913

o, The present sequence represents a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, archritis, multiple sclerosis, autoimmunity, immune dysfunction and allergy Gaps ó 97.7%; Score 345; DB 3; Length 353; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 353; Conserv Sequence 353 AA;

ALIGNMENTS

us-09-466-778b-11.olig9.rag

Sequence 1394 AA;

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120
                                                                        61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
                                                                                                  121 ONCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
                                                                                                                             180
                                                                                                                                                    181 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 240
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                                                                                                                                                                                                       VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                HARE, Hyaluronic Acid Receptor for Endocytosis, hyaluronan, chondroitin, chondroitin sulphate, extracellular matrix, cartilage, skin, vitreous humour, endocytic receptor; glycosaminoglycan, human.
                        1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                 61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                                                                       121 QNCGSGVVGIVDYGPRPNKSEMWDVPCYRMKDVNCTXKVGYVGDGFSYSGNLLOVLMSFP
                                                                                                                                                                    181 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN
MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                       301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                         301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                                                                                                                         Human Hyaluronic Acid Receptor for Endocytosis, HARE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200181544-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                      RESULT 2
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The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04649, ABA04662, AAA47675 and AAA47684). HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is human HARE

New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related

Claim 20; Fig 33; 263pp; English.

nucleic acid

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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express tunctionally active HARE. The method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The expressing HARE on its surface (e.g. gene therapy). Also described is agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing metastrasis by c preventing interaction between tumour cells having HA, CD or CDS coat and non-tumour cells expressing HARE on its surface. The invention also cessing that its enchod useful for detecting the presence of HA, CD and CDS in captor for endocytosis (HARE)
                                        ö
                                                                                                                  1154 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1213
                                                                             228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; human; gene; ss.
                                                                             169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET
                                        Gaps
                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.
  Length 1394;
                                    0; Indels
                                                                                                                                                                                  1214 LSGRDIEHHLANVSMFFYNDLVNGTTLOTRLGSKLLIT 1251
                                                                                                                                                         229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
27.8%; Score 98; DB 5; L/
100.0%; Pred. No. 3.4e-87;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                              ABG72499 standard; protein; 1416 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2002; 2002WO-US013209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2001; 2001US-00842930.
25-APR-2001; 2001US-0286468P.
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                    Best_Local Similarity 100.0
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weigel JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WEIG/) WEIGEL P H. (WEIG/) WEIGEL J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABX13822
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                                                                                                                                                                                                                                                                                                                                                                          19-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                     ABG72499;
  Query Match
                                                                                                                                                                                                                                                         RESULT 3
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Sequence 1653 AA;

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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) creceptor for endocytosis (HARE) or a cell that does not express functionally active HARE. The method involves using HA molecule, and chondroitin molecule (CD). a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemotherapeutic agent or a radioisocope to cell of an individual, especially a human, cxpressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing metastasis by come of a HA coat, a CD coat and CDS coat and concurrent cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This is the amino acid sequence of a longer version of the human libotha Hyaluronan receptor for endocytosis (HARE) shown in
                                                                                 ö
                                                                                                                                                         1176 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; human.
                                                                                                                   169 SGNLLQVIMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET
                                                                                 0; Gaps
                                     DB 6; Length 1416; 3.4e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
                                                                             0; Indels
                                                                                                                                                                                                                              229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                   27.8%; Score 98; DB 100.0%; Pred. No. 3.4
                                                                                                                                                                                                                                                                                                                                         ABG72514 standard; protein; 1653 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2001; 2001US-00842930.
25-APR-2001; 2001US-0286468P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2002; 2002WO-US013209
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                           Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weigel PH, Weigel JA;
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                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABX13823.
Sequence 1416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200286093-A2.
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                                                                                                                                                                                                                                                                                                                                                                               ABG72514;
                                     Query Match
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ABG72499 (Encoded by ABX13822)

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0;
                                                                                                                            1413 SGNLLOVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the NOV3 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomedulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression. They excitiving mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes in assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                               NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase. Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV10; NOV11; NOV12; NOV14; NOV15; NOV16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and immune disorders.
                                                                                       169 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET
                                                     Gaps
                                                       .
0
                 Length 1653;
                                                     0; Indels
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                                                                                                                                                                                      1473 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 1510
                                                                                                                                                                229 LSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLIT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandes
             Score 98; DB 6; Le
Pred. No. 3.9e-87;
27.8%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Lichenstein H, Vernet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 14-17; 141pp; English.
                                                                                                                                                                                                                                                                                                AAB83359 standard; protein; 244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1999; 99US-0166336P.
29-NOV-1999; 99US-016738EP.
09-MAR-2000; 2000US-0187844P.
16-NOV-2000; 2000US-00715417.
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                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                   98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             NOV3 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-648134/74.
N-PSDB; AAF87114.
           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
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                                                   Matches
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N-PSDB; AAF87119.

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detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in Sasays to identify modulators of NOVX expression and activity. The anti-NOVX Abs and antagonist are used to down regulate expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV7, NOV9-11 and NOV1-16 have casein kinase II phosphorylation sites characteristic of serine-threonine kinases. and are used to treat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) like super family and are involved in, e.g. regulation of cell structure and motility and protein management, and are used to treat cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome and marfan syndrome
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Sequence 244 AA;

ö 145 MIGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 204 9 1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 0; Gaps Length 244; Indels 26.3%; Score 93; DB 4; Le 100.0%; Pred. No. 6.6e-83; tive 0; Mismatches 0; 205 RSPLGQYKLTFDKAREACANEAATMATYNOLSY 237 93 61 RSPLGQYKLTFDKAREACANEAATMATYNOLSY Local Similarity 100. Query Match Matches ð

AAB83364 standard; protein; 669 AA. AAB83364; AAB83364

26-MAR-2002 (first entry)

NOV8 protein sequence.

NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular prolliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV10; NOV11; NOV12; NOV14; NOV15; NOV16;

Unidentified

WO200136638-A2.

25-MAY-2001

19-NOV-1999; 99US-0166336P. 29-NOV-1999; 99US-016795EP. 08-MAR-2000; 2000US-0187944P. 16-NOV-2000; 2000US-00715417.

17-NOV-2000; 2000WO-US031543.

(CURA-) CURAGEN CORP.

NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jephers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV9; NOV10;

26-MAR-2002 (first entry)

NOV6 protein sequence.

Fernandes E; Vernet C, Shimkets RA, Lichenstein H,

WPI; 2001-648134/74.

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This sequence is the NOVB protein. The invention relates to the NOV1-
NOV16 proteins, and their coding sequences. The proteins have Cytostatic;
contraceptive; antiinflammatory; immunoadulatory; and cardiovascular
activities. The sequences may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate NOVX expression. They
cretifying mutations or deletions in a patient's genome that affect the
activity of protein by expressing inactive proteins or to supplement the
patients own production of protein. They are used to produce NOVX
cretifying mutations or deletions in They are used to produce NOVX
cretifying mutations of protein. They are used to produce NOVX
cretifying mutations of protein. They are used to wish also be used
activity of protein. The DNA may be used as DNA probes in assays to
detect and quantitate the presence of similar DNAs in samples, and which
patients may need restrative therapy. The NOVX protein may also be used
as antigens in the production of antibodise (Abs) against NOVX and in
assays to identify modulators of NOVX expression and activity. The anti-
NOVX Abs and antagonist are used for detecting the presence of NOVX
in samples. Disorders that may be prevented, diagnosed and/or treated
activity. The anti-NOVX Abs are used for detecting the presence of NOVX
in samples. Disorders that may be prevented, diagnosed and/or treated
corrane/threonine kinases, and are used to treat kinase-related disorders
(e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception).
NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (BGF)
(e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception).
NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (BGF)
-like super family and are involved in, e.g. regulation of cell
development, apoptosis, cell adhesion, growth migration, cell structure
and motility and protein management, and cellular adhesion disorders, immune disorders in decorated and contraception of cell
created and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                               Novel human polypeptides and the nucleic acids that encode them useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                     for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 93; DB 4; L. 100.0%; Pred. No. 1.5e-82; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      626 RSPLGQYKLTFDKAREACANEATMATYNQLSY 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
                                                                                                                                        Claim 1; Page 29-30; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB83362 standard; protein; 669 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syndrome and marfan syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                           immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 669 AA;
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Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                        17-NOV-2000; 2000WO-US031543.
                                                    19-NOV-1999; 99US-0166336P.
29-NOV-1999; 99US-0167785P.
08-MAR-2000; 2000US-0187844P.
16-NOV-2000; 2000US-015417.
                                                                                              Shimkets RA, Lichenstein H,
                                                                                  (CURA-) CURAGEN CORP.
                                                                                                         WPI; 2001-648134/74.
                                                                                                                                       immune disorders.
                                                                                                               N-PSDB; AAF87117
                                                                                                                                                                                                                                                                                                                                                    Sequence 669 AA;
                 WO200136638-A2.
                             25-MAY-2001
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erine/threonine kinases, and are used to treat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) like super family and are involved in, e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT MIGPGRHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 625 9 1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 0; Gaps 26.3%; Score 93; DB 4; Length 669; Indels . 0 1.5e-82; 61 RSPLGQYKLTFDKAREACANEAATMATYNOLSY 93 100.0%; Preq. syndrome and marfan syndrome Conservative Local Similarity tes 93; Conserv Query Match Best Loca Matches ð g ð

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease

Claim 54; Page 25; 363pp; English.

or Alzheimer's disease.

WPI; 2002-666903/71.

Rothenberg M;

N-PSDB; ABT08489

Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U, Shenoy S, Sytvek KA, Gangolli E, Miller C, Boldog F, Li L; Taupjer RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD; Tchernev V, Si J, Edinger S, Stone D, Sciore P, Miller I;

The present invention provides the protein and coding sequences of several novel human proteins, designated NoWX. These can be used in the treatment of diseases such as cancer, Hodgkin's disease, Von Hippellindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, Lesch-Nyhan syndrome, multiple sclerosis, azaxia telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, inflammatory bowel disease,

This sequence is the NOV6 protein. The invention relates to the NOV1
NOV16 proteins, and their coding sequences. The proteins have Cytostatic;

NOV16 proteins, and their coding sequences. The proteins have Cytostatic;

Contraceptive; antiinflammatory; immunomodulatory; and cardiovascular

activities. The sequences may be used in the prevention, diagnosis and

treatment of diseases associated with inappropriate NoVX expression. They

creatifying mutations or delations in a patient's genome that affect the

cativity of protein by expressing inactive proteins or to supplement the

patients own production of protein. They are used to produce NoVX

CC patients own production of protein. They are used to produce NoVX

CC proteins, by inserting the nucleic acid into a cell and culturing it to

express the protein. The DNA may be used as DNA probes in assays to

detect and quantitate the presence of similar DNAs in samples, and which

captients may need restorative therapy. The NOVX protein may also be used

as antigens in the production of antibodies (Abs) against NOVX and in

assays to identify modulators of NOVX expression and activity. The anti
NOVX Abs and antagonist are used to down regulate expression and

activity. The anti-NOVX has are used to down regulate expression and

cutivity. The anti-NOVX has are used to down regulate expression and

cutivity. The anti-NOVX has are used to down regulate expression and

cutivity. The anti-NOVX has are used to down regulate expression and

cutivity. The anti-NOVX has are used to down sequenced, diagnosed and/or treated

cutivity. The anti-NOVX protein. NOV1, NOV3, NOV7, NOV9-11 and

NOV13-16 have casein Khanse II phosphorylation sites characteristic of

contracted the procession and activity is and provenced and nove treated to a season the nove the presence of the presence of nove the nove of th Claim 1; Page 24-25; 141pp; English.

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/note= "optionally Cys depending on polymorphism present in coding sequence"
                                                                                                                                                                                                                                                                     note= "optionally Leu depending on polymorphism present
                                                                                                                                                                                                                                                                                                       'note= "optionally Tyr depending on polymorphism present
                                                                                                                                                                                                                                                                                                                                      'note= "optionally Gly depending on polymorphism present
                                                                                                        Human; NOVX; Bingle nucleotide polymorphism; SNP; anti-HIV; cytostatic;
                                                                                                                 antiarteriosclerotic, antidiabetic, antiantic, antinflammatory; haemostatic; hypotensive; neuroprotective; anotectic; nootropic; antidepressant; immunosuppressive; antibacterial; antiparasitic; orincide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
                                                                                    Human novel protein NOV1c SEQ ID NO: 211.
                                                                                                                                                                                                                                                                                                                 in coding sequence"
                                                                                                                                                                                                                                                                                                                                                  in coding sequence"
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                  .n coding sequence"
                    ABJ10588 standard; protein; 897 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001; 2001US-0262959P.
28-FEB-2001; 2001US-0272408P.
20-APR-2001; 2001US-0285189P.
26-JUL-2001; 2001US-0311266P.
                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-2001; 2001WO-US050076.
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                            Misc-difference 325
                                                                                                                                                                                                                                                                                                                           Misc-difference 832
                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                      WO200259315-A2
                                                                                                                                                                         antiaddictive.
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2000;
                                                              28-NOV-2002
                                        ABJ10588;
RESULT 8
           ABJ10588
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Fernandes E;

Vernet C,

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0;
                                                                                                                                                                                                                               489 MIGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 548
                                                                                                                                                                                             MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; NOVX; single nucleotide polymorphism, SNP; anti-HIV; cytostatic; antiatreriosclerotic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic; nootropic; antidepressant; immunosuppressive, antibacterial; antiparasitic; virucide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
             diabetes, panoreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The present sequence is a protein of the
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colman SD;
     haemophilia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malyankar U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyanka
Shenoy S, Spytek KA, Gangolli E, Miller C, Boldog F, Li L
Taupier RJ, Kekuda R, Santthson G, Zerhusen BD, Liu X, Colr
Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I,
                                                                                                                                  Length 897;
                                                                                                                             26.3%; Score 93; DB 5; Length 897
100.0%; Pred. No. 2e-82;
iive 0; Mismatches 0; Indels
     scleroderma,
                                                                                                                                                                                                                                                                                            549 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 581
                                                                                                                                                                                                                                                                93
atherosclerosis, hypertension,
                                                                                                                                                                                                                                                              RSPLGQYKLTFDKAREACANEAATMATYNQLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel protein NOV1b SEQ ID NO: 4.
                                                                                                                                                                                                                                                                                                                                                                             ABJ10587 standard; protein; 2420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 23-24; 363pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2000; 2000US-025619P.
19-ANN-2001; 2001US-0262959P.
28-FEB-2001; 2001US-02740BP.
20-APR-2001; 2001US-0285189P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2001; 2001WO-US050076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001; 2001US-0311266P
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2002 (first entry)
                                                                                                                                                              93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-666903/71.
                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-666903/
N-PSDB; ABT08488.
                                                                                              Sequence 897 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200259315-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiaddictive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothenberg M;
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infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001;
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                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                               ABJ10587;
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                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic; nootropic; antidepressant; immunosuppressive; antibacterial; antiparasitic; virucide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
 several novel human proteins, designated NOVX. These can be used in the
                                                                                           pain,
              treatment of diseases such as cancers. Hodgkin's disease, von Hipperlindade syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, stroke, tuberous sclerosis, palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia telangiectasia, leukodystrophies, addiction, anxiety, depression, pain obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetees, pantoreatitis, autoimune disease, asthma, arthritis, immunodeficiencies, HIV, viral, becterial or parasitic infections, or graft-versus-host disease. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                  1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spytek KA, Gangolli E, Miller C, Boldog F, Li L;
Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;
Si J, Edinger S, Stone D, Sciore P, Millet I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Casman SJ, Malyankar U;
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                                                                                                                                                                                                                                                              26.3%; Score 93; DB 5; Length 2420; 100.0%; Pred. No. 4.5e-82;
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  2310 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 2342
                                                                                                                                                                                                                                                                                                                                                                                                      61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
                                                                                                                                                                                                                                                                        100.0%; Preq. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patturajan M, Vernet CAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human novel protein NOV1a SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ10586 standard; protein; 2675 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001, 2001US-0262959P.
28-FEB-2001; 2001US-0272408P
20-APR-2001, 2001US-0285189P.
26-JUL-2001; 2001US-0308039P.
09-AUG-2001; 2001US-0311266P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2001; 2001WO-US050076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0256619P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                               93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenoy S, Spytek ka
Taupier RJ, Kekuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-666903/71.
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                            Sequence 2420 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABT08487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiaddictive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rothenberg M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ10586;
                                                                                                                                                                                                                                                             Query Match
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New isolated NOVX polypeptides and polynucleotides, useful

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, open reading frame; ORFX; detection; cytostatic; hepatotropic; vantherary; antipartic; antiparkinsonian; noctropic; neuroptotective; anticorvuleant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; antiariately dermatological; immunosuppressive; antidiammatory; antivital; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; allergy; aplastic anmanodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease or Alzheimer's disease.
                                                                                                                       The present invention provides the protein and coding sequences of several novel human proteins, designated NOVX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-Lindau syndrome, Alzheimer's disease, turberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Whyan syndrome, multiple sclerosis, ataxia telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft, versus-host disease. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.3%; Score 93; DB 5; Length 2675; 100.0%; Pred. No. 4.9e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2363 RSPLGOYKLTFDKAREACANEAATMATYNOLSY 2395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RSPLGQYKLTFDKAREACANEAATMATYNQLSY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB42164 standard; protein; 330 AA
                                                                                     Claim 1; Page 20; 363pp; English.
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02-APR-1999; 99US-0127636P.
30-APR-2009; 200US-00549769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000WO-US008621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2675 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                                                                                                                                                                invention
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AAC7446 to AAC77606 encode the proteins given in ABB40237 to AABB43397,
which represent the human ORRX open reading frames 1 to 3161. The ORFX
cequences have activities such as: cytostatic; hepatotropic, vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolyvic; coagulant; vasotropic; antidiabelic; hypotensive;
dermatological; immunosuppressive; antinhtamatory; antibacterial;
antiviral; antifungal; antirheumatic; antithyroid; and antiansemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
to, or preventing or treating pathological conditions associated with an
to, or preventing or treating pathological conditions associated with an
to, or preventing or treating pathological conditions associated with an
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to, or preventing pathological conditions and
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to antipace properties of the proteins and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 SGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENET 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase. Peutz-Jephers syndrome; cellular prolliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-OT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV9; NOV10;
                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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                                                                                                                                                                                                                                                                                                        Claim 11; Page 3007-3008; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 LSGRDIEHHLANVSMFFYNDLVNGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 LSGRDIEHHLANVSMFFYNDLVNGT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB83358 standard; protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                    Shimkets RA, Leach M;
(CURA-) CURAGEN CORP.
                                                                                                        2000-602362/57.
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                                                                                                                                N-PSDB; AAC76373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB83358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB83358
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This sequence is the NOV2 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the procein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, and which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVX Abs and antagonist are used to down regulate expression and activity. The anti-NoVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/thronine kinases, and are used to treat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (BGF)-like supper family and are involved in, e.g. regulation of cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders nov6-like fibrillin proteins and are used to treat cancers, treat candiovascular disease e.g. hypertrophic cardiowpoathy, long-QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patients may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in assays to identify modulators of NOVX expression and activity. The anti-
                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                     Fernandes E;
                                                                                                                                                                                                                                                                     Vernet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 10-13; 141pp; English.
                                                                                                                   29-NOV-1999; 99US-0167785P.
08-MAR-2000; 2000US-0187844P.
16-NOV-2000; 2000US-00715417.
                                                                                                                                                                                                                                                                   Shimkets RA, Lichenstein H,
                                                                                            99US-0166336P
                                              17-NOV-2000; 2000WO-US031543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome and marfan syndrome
                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                    WPI; 2001-648134/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                               .mmune disorders.
                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF87113
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                                                                                              19-NOV-1999;
25-MAY-2001.
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tise inversion in the individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express that the functionally active HARE. The method involves using HA molecule, and chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The certhod is useful for targeting a compound, preferably a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least on of a HA coat, a CD coat and a cell expressing HARE on its sucreace. This second method is useful for preventing interaction between tumour cells having HA, CD or CDS coat and con-tumour cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This sequence represents the LINK domain of the human cells than may be present in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; vitreous humour; endocytic receptor; glycosaminoglycan; rat.
               Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; human; LINK domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a method of targeting a compound to a cell or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 QKAKYHLCSAGWLETGRVAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 QKAKYHLCSAGWLETGRVAYPTAFASQNCGSGVVGIVDYGPRFNKSEMWDVFCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM47675 standard; protein; 1431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 77; 167pp; English.
                                                                                                                                                                                                                                25-APR-2002; 2002WO-US013209.
                                                                                                                                                                                                                                                                         25-APR-2001; 2001US-00842930.
25-APR-2001; 2001US-0286468P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other HARE-like proteins
                                                                                                                                                                                                                                                                                                                                                                                                    Weigel JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-093126/08.
                                                                                                                                                                                                                                                                                                                                       (WEIG/) WEIGEL P H. (WEIG/) WEIGEL J A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 93 AA;
                                                                                                                                               WO200286093-A2.
                                                                                                       Homo sapiens
                                                                                                                                                                                        31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                    Weigel PH,
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Homo sapiens.
                    Weigel PH,
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                                                                                                                                                                                                                                                                                                            Query Match
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                     AAU00893
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                                                                                                                                                                                                                                         The present invention relates to sequences for rat and human HARE (Hyaluconic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAM47675 and AAM47684). HARE can bind specifically to at least one of hyaluconic acid (HA, also known as hyaluconan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is rat HARE
                                                                                                                                                                                         endocytosis, useful e.g. for hyaluronic acid, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; rat; receptor.
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                . 0
                                                                                                                                                                                                                                                                                                                                            7.1%; Score 25; DB 5; Length 1431;
100.0%; Pred. No. 2.7e-15;
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
                                                                                                                                                                                        New mammalian hyaluronic acid receptor for identifying agents that inhibit binding to
                                                                                                                                                                                                                                                                                                                                                100.08; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                               1057 FQDTTVGVFHLRSPLGQYKLTFDKA 1081
                                                                                                                                                                                                                                                                                                                                                                                50 FODTIVGVEHLRSPLGOYKLIFDKA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG72498 standard; protein; 1431 AA
                                                                                                                                                                                                                           Claim 20; Fig 21; 263pp; English.
                                                                                                                                             Weigel JA;
                                                             25-APR-2001; 2001WO-US013403.
                                                                             25-APR-2000; 2000US-0199538P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2002; 2002WO-US013209.
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25-APR-2001; 2001US-0286468P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                            Weigel PA, Zhou B,
                                                                                                                                                             WPI; 2002-049271/06
                                                                                                       (WEIG/) WEIGEL P A.
                                                                                                                        (WEIG/) WEIGEL J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WEIG/) WEIGEL P H.
          Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                           Sequence 1431 AA;
                                                                                                                                                                       N-PSDB; ABA04648
                          WO200181544-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200286093-A2.
                                                                                                                                                                                                         nucleic acid.
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                                            01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG72498;
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                              Matches
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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) creceptor for endocytosis (HARE) or a cell that does not express functionally active HARE. The method involves using HA molecule, and/or chondrottin molecule (CD), a chondrottin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The chond is useful for targeting a compound, preferably, a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a cone of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing metastasis by preventing interaction between tumour cells having HA, CD or CDS coat and contunuour cells expressing HARE on its surface. The invention also concerning content of the surface of the coat and cDS in a biological fluid. This is the amino acid sequence of the rat 175kDa cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer related protein; food additive; preservative; immunogen; antibody; bone cancer; adrenal cancer; bone marrow cancer; breast cancer; gastrointestinal cancer; liver cancer; lung cancer; urogenital cancer; immune disorder; Addison's disease; allergy; diabetes mellitus; autoimmune haemolytic anaemia; autoimmune thyroiditis; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; acquired immunodeficiency syndrome; AIDS; cardiovascular disorder; parkinson's disease; wound healing; neurological disorder; parkinson's disease; Albeimer's disease, cerebral anoxia; epilepsy; viral infection; bacterial infection; fungal infection; epilepsy; parasitic infection; agonist; antagonist.
                                                                                                                                                                                                                                                                Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%; Score 25; DB 6; Length 1431; 100.0%; Pred. No. 2.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db c,
. 2.7e-15;
. a 0; Indels
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/label= Immunogenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Immunogenic_epitope
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example, Fig 2; 167pp, English.
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                                                                                 Weigel JA;
                                                                                                                                                      WPI; 2003-093126/08
(WEIG/) WEIGEL J A.
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Matches 25; Conserv
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Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
25-APR-2002; 2002WO-US013209.
                                              25-APR-2001; 2001US-00842930.
25-APR-2001; 2001US-0286468P.
                                                                                                                                                                                      Weigel JA;
                                                                                                                                                                                                                                     WPI; 2003-093126/08.
                                                                                                                 (WEIG/) WEIGEL P H. (WEIG/) WEIGEL J A.
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                                                                                                                                                                                         Weigel PH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a novel Human cancer related protein. The polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condution in e.g. humans, mice, rabbits, goats, cares, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotide are useful for chromosome capabilities. The polynucleotide are useful for chromosome capabilities are useful in the diagnosis, reatment and prevention of antagonists are useful in the diagnosis, reatment and prevention of cancer (e.g. cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital), immune disorders (e.g. Addison's disease, allergies, autoimmune thromoditis, diabetes mellitus, Crohn's disease, multiple autoimmune thryroiditis, diabetes mellitus, Crohn's disease, multiple immunodeficiency syndrome, AIDS), cardiovascular disorders such as myocardial ischaemias, wound healing, neurological diseases (e.g. myocardial ischaemias, wound healing, neurological diseases (e.g. and infectious diseases, Alzheimer's disease, cerebral anoxia and epilepsy) and infectious diseases such as viral, bacterial, fungal and parasitic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD;
chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis;
tumour; gene therapy; human; motif.
                                                                                                                                                                                                                                                                                                                                                                           Twenty nine nucleic acid molecules encoding human cancer associated proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%; Score 20; DB 4; Length 106; 100.0%; Pred. No. 2.6e-11; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 403; 427pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG72512 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 IILVTGAVALAAYSYFRINR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                illyrgavalaaysyrrink 42
                                                                                                                                       99US-0152296P.
99US-0158003P.
                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                           30-AUG-2000; 2000WO-US023794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-2003 (first entry)
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Best Local Similarity
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WO200118014-A1.
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                                              15-MAR-2001
                                                                                                                                                                                                                                                         Roschke V;
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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) creceptor for endocytosis (HARE) or a cell that does not express treceptor for endocytosis (HARE) or a cell that does not express cfunctionally active HARE. The method involves using HA molecule, and/or chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or condition antibody raised against a HA-binding domain of HARE. The condition of a uniformation of an individual, especially a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, conserver and the surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its second method is useful for preventing metastasis by preventing interaction between tumour cells having HA, CD or CDS coat and cDS coat and cDS in contumour cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This sequence represents a putative motif from the human 190kDa Hyaluronan receptor for endocytosis (HARE) that may be present in other HARE-like proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; human; rat; vitreous humour; endocytic receptor; glycosaminoglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 18; DB 6; Length 18; 100.0%; Pred. No. 5.5e-10; tive 0; Mismatches 0; Indels
Claim 23; Page 77; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM47702 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HARE peptide fragment #6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGPGKHKCECKSHYVGDG
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The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04649, ABA04662, AAM47675 and AAM47649. HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in sulphate artillage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is a peptide fragment of HARE, which was used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; human; rat; vitreous humour; endocytic receptor; glycosaminoglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related nucleic acid.
                                                                                                                                   New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related
                                                                                                                                                                                                                                                                                                                                                                                                            4.2%; Score 15; DB 5; Length 15; 100.0%; Pred. No. 4.3e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HARE peptide fragment PR 1825 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM47690 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              4.2.
100.0%; Pre
                                                                                                                                                                                                Example; Page 95; 263pp; English.
                                                                            Weigel JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weigel JA;
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02-NOV-2000; 2000US-0245320P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RSPLGOYKLTFDKAR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RSPLGQYKLTFDKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weigel PA, Zhou B,
                                                                          Zhou B,
                                                                                                        WPI; 2002-049271/06
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              (WEIG/) WEIGEL P A. (ZHOU/) ZHOU B.
                                          WEIG/) WEIGEL J A.
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 AA;
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                                                                                                                                                                 nucleic acid.
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                                                                          PA,
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                                                                          Weigel
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Matches
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                                The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAM47675 and AAM47649. HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is a peptide fragment of HARE, which was used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue of an individual expressing a functionally active hydranoran (HA) receptor for endocytosis (HARE) or a cell that does not express functionally active HARE. The method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemotherapeutic expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing inceraction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD;
chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis;
tumour; gene therapy; human; motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a method of targeting a compound to a cell or
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 190kDa Hyaluronan receptor for endocytosis putative motif #13.
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                                                                                                                                                                                                                                                                       3.7%; Score 13; DB 5; Length 13; 100.0%; Pred. No. 3.5e-05; ive 0; Mismatches 0; Indels
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Example; Page 94; 263pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2001; 2001US-00842930.
25-APR-2001; 2001US-0286468P.
                                                                                                                                                                                                                                                                                                                                                     213 GTLFVPQNSGLGE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       1 GTLFVPONSGLGE 13
                                                                                                                                                                                                                                                                                                                13; Conservative
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                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                  Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200286093-A2.
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                                                                                                                                                                                                                                                                         Query Match
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Gaps . 0

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its surface. This second method is useful for preventing metastasis by preventing interaction between tumour cells having HA, CD or CDS coat and non-tumour calls expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This sequence represents a putative motif from the human 190kDa Hyaluronan receptor for endocytosis (HARE) that may be present in other HARE-like proteins
     88888888%8
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Sequence 13 AA;

ö 0; Gaps Query Match 3.7%; Score 13; DB 6; Length 13; Best Local Similarity 100.0%; Pred. No. 3.5e-05; Matches 13; Conservative 0; Mismatches 0; Indels

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Search completed: April 1, 2004, 09:56:56 Job time : 59 8ecs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

April 1, 2004, 09:56:50; Search time 3238 Seconds (without alignments) 3255.513 Million cell updates/sec

Run on:

1 MTGPGKHKCECKSHYVGDGL.....ALAAYSYFRINRKTIGFXHF 353 US-09-466-778B-11 1865 Perfect score: Sequence:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

27513289 segs, 14931090276 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/USG9466778/runat_01042004_095642_10592/app_query.fasta_1.519
-O=/cgn2_1/USPTO_spool/USG9466778/runat_FMINATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UOTANG=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USFR=USG9466778 @CGN 1 1 3437 @runat_01042004_095642_10592 -NCFU=6 -ICFU=3
-NO MAAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMBOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPORT=0.5 -DELOP=6 -DELEXT=7

EST: * Database :

em_estba:*
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em gas hum:* em gas inv:* em_gae_pln:* fun:* ет двв_тат:* en htts: *c gb_est1: * gb_est2: * gb_est3: * gb_est4: * gb_est4: * em_estfun:* em estom: * em_988_ em_988_

em gss mus: *
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em gss rod: * em_gss_phg:* em_gss_vrl:* gb_gssl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	AK034522 Mus 1	76384	23552	3247	3027	9778	2486	9712	# F	1 6	774	705197	12417	51168	59001	00/24	045I	10000	30769	897	57207	38989	69767	26658	35659	322	52129	31159	81146	47090	44644		70695	94227	926	54659	12246	31025	AW595426 Ek37g02.y	35766 SS1-007	47334 678437	
B ID	11 AK03452	11/1/A2 0	BU52355	BC04924	1 CK02802	3 BX73977	BI83248	L BC01971	1 T47504		CB26877	BX70519	4 CA34241	3 BX86116	4 CD35900	D BF34270	0 BF30045) BE23322	2 BM23862	E EXC3078	2 BM76720	9 CNS03DE	2 BM76976	3 BX86665	0 AW43565	3 BQ88432	4 CA36212	2 BM18115	2 BM18114	2 BI90602	2 BI14464	DITSC#O	O CNSUSAI	DE EM 69422	2 BM76976	4 CA36465	2 BG71224	3 BO13102	0 AW59542	2 BG93576	4 CA34733	
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ALIGNMENTS

linear HTC 18-SEP-2003

AK034522 3085 bp mRNA linear HTC 18-SEP-2 MLS masculus adult male diencephalon CDNA, RIKEM full-length enriched library, clone:9330210123 product:similar to CD44-LIKE PRECURSOR FELL (Homo sapiens), full insert sequence. AK034522 AK034522.1 GI:26330004 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 1 AK034522

HTC; CAP trapper. Mus musculus (house mouse)

ORGANISM

Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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/translation="GRYHVVACQQLLLENLKVITSATTLQGEPISISVSQDTVLINKK
AKVLSSDISTNGVIHVIDTLLSPQNLLITPKGASGRVLLNLTTVAANHGYTKESKLI
QDSGLLKVITDPMHTPVTLFWFTDKALQALPQEQQPFLFUEDNKDKLKAYLKFHVIRD
HALASDLFRSASWRTLQGSELSVRCGTGSDVGELFINGQMCRIIQRRLLFDGGVAYG
IDCLLMDPTBGGRCDTFTTFNIPGEGSCFFFFFFINGWCRIYKKCIYNPLDFRRD
VBGCQNLCTLVVHVPRCCSGGYFMFDCQACFGGPDTPCNNRGMCYDQYKFTGQCQCHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENCTACELCLPGREGEDCOPCGCSERGOCDEGITGSGQCLCEAGWTGRECDAPTVVIP
VCIPACSMHATCMENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVS
CSCQKGYKGDGHSCTEIDPCANGVNGGCHEHATCRWTGPGKQKCECKSHYVGDGRDCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEGIPLDRCLIQDNGCCHPDANCVDLHRQDTTVGVFHLRSPLGQYKLTPDKAKEACAKE
AASIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTIYASKKCANIVGIVDYGTRTNKS
EMMDVPCYRMKDVNCTCKAGYVGDGFSCNGNLLQVLMSFPSLTNFLTEVLVFSRSSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRAFLKHLTDLSISGTLFVPQNSGLPKNKSLSGRDIEHHLTNVNVSFYDDLVNGTVLK
TRLGSGLLTTSSQDQLHQBARFVDGRAILGMOILASNGVLHTISBPLKAPPTAATASH
SGLGTGIFCAVVLVTGALALAAYSYFRLNQRTTGFRRFESEDDIDALAFGKQQPESIT
NPLYBTSTPAAREPSCDFFTDSGERELENSDPLGALRS"
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                                                                                                     /tissue type="diencephalon"
/clone lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                    /note="unnamed protein product; putative similar to CD44-LIKE PRECURSOR FELL [Homo sapiens] (SPTR[Q9NRY3, evidence: FASTY, 78.1%ID, 99.4%length, match=673]"
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/db_xref="GI:26330005"
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                     /db_xref="taxon:10090"
/clone="9330210123"
                                                                                                                                                                   /dev_stage="adult"
<1. .2685
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                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okzzaki, Y., Muramatsu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamananco, R., Matsunco, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hiramoto, K., Hiramoka, T., Hirozane, T., Hari, F., Imotani, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakanura, M., Nishi, K., Nomura, K., Nimazaki, R., Ohno, M., Ohno, M., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakaume, N., Sano, H., Saaaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takabashi, F., Takku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
Nature 420, 563-573 (2002)

6 (bases 1 to 3085)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sagaki, N., Carninci, P.
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                  Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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URL:http://fantom.gsc.riken.go.jp/
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/strain="C57BL/6J"
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  pCS107 with
embryos. Ecori-Noti cut cDNA was then ligated Ecori at the 5' end and Noti at the 3' end. Vector: pCSIO7; Site_1: EcoR; Site_2: Noti Host: Escherichia coli DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                     819
179
37
51
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                             organism="Silurana tropicalis"
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Matches:
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963.00
79.12%
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51.64%
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TTpA026k09 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2410 GGCATATTCTGCGCTGTCGTCCTGGTTACTGGTGCGATTGCTCTGGCTGCCTACTCCTAC 2469
      1816 AAGAAATGT---GCAAACATTGTGGGGGATTGTAGACTACGGAACCAGGACCAACAAGAGT 1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerArg***LeuLyBAlaProProAlaProValThrLeu***HisThrGlyLeuGly*** 320
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                                                                                                                               TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro 180
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                               1993 reacreaceaacrrecreacaeacrecrecrecrecritriceaeaacreaceceae
                                               GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly
                                                                                                                                                                                                                 SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerAlaArgGlyArg
                                                                                                                                                                                                                                                                                                   AlaPheLeuGluHiBLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn
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TROPICALIS_SEQUENCE_ID: TTPA026k09.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
CDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX717115 MGC-tadpole Silurana tropicalis cDNA clone mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinxton, Cambridgeshire, CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: trop@sanger.ac.uk
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BX717115
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09-AUG-2002
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Cryzias latipes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                   483
                                                                      304 TTTGGTCACGTGGGCATCGTAGACTACGGCTTACGCAACAACCTCAGTGAGACCTGGGAC 363
                                                                                                                                                                                                                                                                                                145 ValpheCysTyrArgMetLysAspValAsnCysThr***LysValGlyTyrValGlyAsp 164
                                                                                                                                                                                                                                                                                                                                        364 ACCTICIGCIACAGGGICAAGGAGGICAAAIGIGAAIGIAAAGCAGGIIAIAIAGGAGAI 423
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Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
124 GGACAGTACAAGCTGAACTATACATCGGCCCAGGAGGCCTGCACAGGAGAGGGGGGAACC 183
                                            85 MetalaThrTyrAsnGlnLeuSerTyr***GlnLy8AlaLysTyrHisLeuCysSerAla 104
                                                                                                                             105 GlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGlnAsnCysGly 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tadagu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:8090"
60.1cm="wrkf01SsB002F09"
6ex="mixture of female and male"
/Lissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryzias latipes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 PheTyrAsnAspLeuValAsnGlyThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="Hd-rR"
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BJ523552.1 GI:22182364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 GlyGlnTyrLygLeuThrPheAspLysAlaArgGluAlaCysAlaAsnGluAlaAlaThr 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.

1. (bases 1 to 694)

Rexroad, C.E. and Keele, J.W.
Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 CyeValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeuArgSerProLeu 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross match v0.999129.
Seq primer: AGCGGATAACAATTTCACACAGGA.
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                                 LeuGlnThrArgLeuGlySerLysLeuLeuIleThrAspArgGlnAspProLeuHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kerneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
        GluHisHisLeuAlaAsnValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2:
Library made from pooled tissue from brain, gill,
splean, muscle, and kidney."
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="1RT35N18 D G09"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-466-778B-11 (1-353) x CA376384 (1-694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      CA376384.1 GI:24694516
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55.02%
38.50%
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                                                                                                                                                                                                                                                                                                                                                                     CA376384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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           235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                             RESULT 3
CA376384
                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
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Alignment Scores:

ORIGIN

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Contact: nisc mgc@nhgri.nih.gov,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R. w., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,N. i., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Ysurgeon,C., Vogf,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1612 Accediccerracececeristrateccacerracerraceraceracercarescracers 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1672 TGTCTAGAGGAGCTTGAACCCCCTGTGGACAGATGCTTGGGAGGATCATCACCTTGCCAC 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1732 ACTGATGCTTTGTGCACTGACCTACATTTCCAGGAAAAACAGGCTGGTGTCTTCCACATC 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1792 CAGGCCACCAGTGGCCCTTATGGTCTGACCTTCTCAGAGGCCACGGAAGCGTGTGAGGGC 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: RRAE Plate: 99 Row: g Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
       31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 Cys---GluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Mammary tumor metastatized to lung. Transe spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone lib="NOI CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone has the following problem: frame shifted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3025
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146
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                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                        Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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/mol_type="mRNA"
/strain="CZECH II"
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/clone="IMAGE:5038209"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly 160
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Direct Submission
Submitted (21-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                          1 MetThrGlyProGlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeu
                                                                                                                                                                                                                                                                                                                                                            272 GAGGGAGGGTCCTTGGCCACGCTCCCCAGCTTCACCATGCTCAGCAGGGGGCCTTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                           21 AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis
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Mus musculus, Similar to stabilin 1, clone IMAGE:5036209, mRNA
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Mismatches:
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Matches:
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clone_lib="MF01SSB cDNA"
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Mammalia; Butheria; Rodentia;
1 (bases 1 to 3025)
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                                                                                               3.59e-75
703.00
73.73%
56.68%
37.69%
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                                                                                                                                                                           Best Local Similarity:
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BC049247

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 5 BC049247

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SOURCE ORGANISM

TITLE JOURNAL AUTHORS REFERENCE

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Similarity:
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Best Local Similari
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AGENCOURT_16620198 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7053029
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                                                                                                                                                                                                                                  161 TyrvalglyaspglyPheSer---TyrSerGlyAsnLeuLeuglnValLeuMetSerPhe 179
                                                                                                                                                                                                                                                                                                           180 ProSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGly 199
                  LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer 120
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Actinopteryqii, Neopterygii, Teleostei, Ostariophysi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AsnValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeu
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                         121 GlnAsnCysGlySerGlyValValGlyIleValAspTyrGlyProArgProAsnLysSer
                                                                                                                                                              GlumetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly
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Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1122)
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/clone libe Will GC_7"
//note="Weetor: pExpress!; Site_1: Not1; Site_2: EcoRV;
//note="Weetor: pExpress!; Site_1: Not1; Site_2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH ZGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsnGlu
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                                                                            National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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/tissue_type="whole_body"
/lab_host="DH10B"
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:7955"
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BX739778

722 bp mRNA linear EST 18-NOV-2003
BX739778 XGC-tadpole Silurana tropicalis cDNA clone TTpA048d24 5',
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MetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGlyTyr 161
                                                                                               ValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPheProSer 181
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Email: trop@sanger.ac.uk
Sanger Kenopus tropicalis EST project 2001
TROPICALIS_ENGURICE ID: TTpA048d24.plkaSP6
Sequencing primer: $P6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dr primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
Vector: pCS107; Site 1: EcoRI, Site 2: NotI
HOBE: Escherichia coli DH10B.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                       222 GlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsnVal
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Sanger Institute
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b1842486
603082278F1 NIH_MGC_120 Homo sapiens CDNA clone IMAGE:5221410 5',
mRNA sequence.
/dev_stage="tadpole (stage 35-40)"
/Lab host="E. coli DH108"
/clone lib="XGC-tadpole"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sig of poly A+ RNA from tadpole embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTGCTGCAAGTCTTGACATCTTTTCTTTTCAAATTTCCTTACGGAAATTTTGGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 LeuHisPro-------ThrGluThrArgCysValAspGlyArgAspThr 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 LeuGluTrpAsplleCysAlaSerAsnGlyIleThrHisValIleSerArg***LeuLys 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 TIGCAGIGGGACATTAICGCITCCAAIGGAAICAITCACACAATIGCIGAACCICTAACT 480
                                                                                                                                                                                                                                                                                                                                                                      09
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                                                                                                                                                                                                                                                                                                                                                         1 GATGTGTCATGTATTTGCAAACCTCCCTTTGTGGGGAGATGGCTACACTTGTAATGGAAAC
                                                                                                                                                                                                                                                                                                                              152 AspvalAsnCysThr***LysValGlyTyrValGlyAspGlyPheSerTyrSerGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 TyrSerAsnSerSerAlaArgGlyArgAlaPheLeuGluHisLeuThrAspLeuSerIle
                                                                                                                                                                                                                                                                                                                                                                                                   172 LeuLeuGlnValLeuMetSerPheProSerLeuThrAsnPheLeuThrGluValLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 ArgGlyThrLeuPheValProGlnAsnSerGlyLeuGlyGluAsnGluThrLeuSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 AlaProProAlaProValThrLeu***HisThrGlyLeuGly***GlyIlePhe*****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 IlelleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyrPheArglleAsnArg
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Matches:
Conservative:
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Indels:
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KEYWORDS
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRMK plate: 40 Row: d Column: 23 This clone has the following problem: frame shifted. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTC 20-SEP-2002
                                                                                                                                                                                 673 CCAGGAAGTGCTGGCCTATTCCAACAGCTCAGCTCGAGGCCGTGCATTTCTAGAACAACT 732
                                                                                                                                                                                                                                     uThrAspLeuSerlleArgGlyThrLeuPheValProGlnAsnSerGlyLeuGlyGluAs 226
                                                                                                                                                                                                                                                                613 ITCAGCCACCCAGGTCCCTGCACACCAGGCTGGCCCCTCTGATGACCTCCTTCTTCTCC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC019712 20-SEP-
Mus musculus, Similar to stabilin 1, clone IMAGE:3663004, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="Mammary tumor metastatized to lung.
MMTV-LIE/Wntl model, Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Younaratne, P.H., garla, A.M., Lu, X., Hulyk, S.W., Hale, S.N.
Yoon, V.S., Kowlis, C.R., Lawrence, S., Martin, R.G., Muzny, I Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2368
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/lab_host="DH10B"
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/clone="IMAGE:3663004"
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/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC019712.1 GI:22507492
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43.72%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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BC019712
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KEYWORDS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db zref="taxon:9606"
/clone=lineMGE:5221410"
/lab host="lmH108"
/clone lib="NNH MGC 120"
/clone lib="NNH MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORTE; Site l: Not; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1:5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gubber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 LeuSerTyr***GlnLysAlaLysTyrHisLeuCysSerAlaGlyTrpLeuGluThrGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 cederreccraceccacaeccrrceccrccaeaacrerecereregregerreseara 312
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                 Email: cgapDs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11556 row: 1 column: 19
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127
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-466-778B-11 (1-353) x BI832486 (1-793)
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AUTHORS
TITLE
JOURNAL
COMMENT
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274PPOTHIGIUTHIANG	ilevasiasis, olderwood, N., montandam, F., matersom, N., millsom, N. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Generation and analysis of 280,000 human expressed sequence tags 97044478 8889549 Other ESTS: yb14f01.s1 Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1800 Fax: 314 286 1810 Fax: 314 286 1810 Fax: 314 286 1810	
QY QY Db 10 QY Db 11 QY Db 11 QY Db 12 RESULT 10 T47504 LOCUS DB TA7504 LOCUS DB TA7504 COCCESSION WERSION	TITLE JOURNAL MEDLINE PUBMED COMMENT	FEATURES
Best Local Similarity: 32.96\$ Mismatches: 144	170 GlyAsnLeuGlnValLeuMetSerPheProSerLeuThrAsnPheLeuThrGluVal	Qy 227

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prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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/dev stage="0 day neonate"
1. 3454
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="taxon:10090"
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Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631403B18 product:hypothetical Beta-Ig-H3/Fasciclin domain containing protein, full insert sequence.
  /clone lib="Stratagene placenta (#937225)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
BEORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dI. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 TyrSer-GlyAsnLeuLeuGlnValLeuMetSerPheProSerLeuThrAsnPheLeuTh 187
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Matches:
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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557.50
85.06%
83.12%
29.89%
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/note="hypothetical Beta-Ig-H3/Fasciclin domain containing
protein (InterPro|IPR000782, evidence: InterPro)"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yokohama,
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamannoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohasnagawa 230-0045, Japan (8-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp, Tel:81-45-503-9222, Pax:81-45-903-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
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Functional annotation of a full-length mouse cDNA collection
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Please visit our web site for further details.
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:4631403B18"
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2652 272 2712 279 279	Oy 283 ArgAspThrLeuGluTrpAspIleCyshla Db 2831 AGCCACGTCGTCGTGGGACATCATGGCT Oy 303 ***LeuLysAlaProproalaProvaIThr Db 2891 CCACTGCTCATGCCTCCCCAGACTGTGAGT	12 38 38 710 110N 10N DS	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Cr Mammalia; Eutheria; Primates; Ca Margholia; Butheria; Primates; Ca I (bases 1 to 120.1) AUTHORS Li,W.B., Gruber,C., Jessee,J. an TITLE Full-length CDNA libraries and n JOURNAL COLLACT: Genoscope COMMENT Genoscope - Centre National de S BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr.	Library was constructed by Life Invitrogen. This sequence belong more information about this clus http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CinBA011 Feng Liang Email : fliang@lifete http://fulllength.invitrogen.com Faraday Avenue Genoscope sequenc FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers / mol type="mRNA" / mol type="mRNA" / mol type="mRNA" / mol type="mRNA" / mol type="mRNA" / mol type="mRNA" / mol type="mRNA" / mol type="mRNA" / mol type="mRNA"	Action asples (Consection of the Consequence of the
Alignment Scores: 2.02e-55 Length: 3454 Pred. No.: 2.02e-55 Matches: 131 Score: 131 Percent Similarity: 45.70% Monacrvative: 48 Best Local Similarity: 33.50% Mismatches: 126 Query Match: 11 US-09-466-778B-11 (1-353) x AK028441 (1-3454)	B LysCysGluCysLysSerHisTyrValGlyAspGlyLeuAsnCysGluProGluGln 26 :::	Db 1816 CCCCTGTGGACAGATGATCATCACCTTGCCACTGATGCTTTGTGCACT	Qy 1996 TGACTCCCTCAACTCTCTGCCGCCCAACAGCTAGGTTTTCATGCTTCGTGGGCTGG 2055 Qy 107 LeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGlnAsnCygGlySerGly 126 Db 2056 TGGCCAACGCTGCTGCCGCCCAACAGCTAGGTTTCATGCTTCGTGGGCTGG 2055 Qy 107 LeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGlnAsnCygGlySerGly 126 Db 2056 TTGGCCAACGGCTCTGCTGCTGCTCGTCGTCACCCCGGCAGACTGGTAATAT 2115 Qy 127 ValValGlyIleValAspTyrGlyProArgProAsnLySSerGluMetTTpAspValPhe 146 Db 2116 CGTGAAGGTGTAGCCTTGGGGTCGTTAGGAACTCTCGGAAGTTCTAGCTACTAC 2175	147 CysTyrArg	2355 TIGGCGGCACIGCCACCICCACCICCACIGCGGCGCGATGCCCATIGCCATIGCCATIGCCACGCGCACIGCCCACIGCCCACIGCCCACGGCGCACGCGCACGCGCACGCGCGCG

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TTAGCCTCTTCATAGTGACACGGGCCCTGAC 2711
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                        -----CysvalAspGly 282
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Catarrhini, Hominidae, Homo.
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e Technologies, a division of
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572 bp mRNA linear EST 20-FEB-20 mRNA linear EST 20-FEB-20 CDNA 5, mRNA sequence.
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                                                                                                                                         -----AspThrThrValGlyValPheHisLeuArgSerProLeuGlyGlnTyrLysLeu
                            37 GlyGlnCysHisAlaAspAlaLysCysValAspLeuHisPheGln-
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                                                                                                                                                                                                                                                      /tissue type="Adipose"
/clone lib="Human Fat Cell 5'-Stretch Plus
/note="Vector: lambdaTriplEx"
Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
                                                                                                                                                                                                                                                                                                                                           572
86
31
68
22
                          University of Maryland 57, 660 Redwood St, HH497, Baltimore, MD 21201, TEL: 410 706 1672 Fax: 410 706 1622
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                FORWARD: CTCGGGAAGCGCGCCATTGTGTTGGT
BACKWARD: AATACGACTCACTATAGGGCGAATTGG
Seg primer: GTTGGTACCCGGGAATTC.
                                                                                    Email: dgong@medicine.umaryland.edu
                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-466-778B-11 (1-353) x CB268774 (1-572)
                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Male and Female"
                                                                                                                                                                Location/Qualifiers
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462.00
62.57%
45.99%
24.77%
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Query Match:
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EST 20-FEB-2003

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to S7. Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
BST analysis of human adipose gene expression

CB268774.1 GI:28443359 Homo sapiens (human) sapiens

KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

DEFINITION

CB268774

ACCESSION

VERSION

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719 bp mRNA linear EST 05-NOV-2002 mRNA sequence.

CA342417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 ThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHisLeuCysSerAlaGlyTrp 106
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                                                                                                                                                                                       361 ---chigcriddcarddadaharrcrrrddcaridrrcradarcardddcrccrd 417
                        241 ATGACTCCAACAAGATATGTGGATGGAAAACCTATTTTGCAGTGGGACATTATCGCTTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. I (bases i to 719)
Rexroad, C.B. and Keele, J.W. Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross match v0.990329.
Seq primer: AGCGGATAACAATTTCACACAGGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TACCAGCTGAACTACACCGATGCTGAGCTAGCCTGTCAAGGGGGGGCTACGCTCGCC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NGCCWA 1RT"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library from brain, gill, liver.
spleen, muscle, and kidney."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 TyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsnGluAlaAlaThrMetAla
                                                                                           301 AATGGAATCATTCACACAATTGCTGAACCTCTAACTGGGCCTCCAGAGCCATTAGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetcwn Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
                                                               294 AsnGlyIleThrHisValIleSerArg***LeuLysAlaProProAlaProValThrLeu
                                                                                                                                                                                                                              334 AlaLeuAlaAlaTyrSerTyrPheArglleAsnArgLysThrlleGlyPhe 350
                                                                                                                                                                                                                                                                        418 GCACTCGCAGTATACTATTATAAGAAGTTCAACAGAAAAGATTTCCAATTC 468
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96
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Indels:
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Matches:
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Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT32P18_D_H09"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-466-778B-11 (1-353) x CA342417 (1-719)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                              CA342417.1 GI:24587588
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56.90%
40.17%
23.65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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DB:
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TITLE
JOURNAL
COMMENT
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CA342417
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KEYWORDS
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                                                BX705197 865 bp mRNA linear EST 17-NOV-2003
BX705197 XGC-tadpole Silurana tropicalis cDNA clone TTpA006003 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCSl07; Site_1: EcoR1; Site_2: Not1; cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole embryos. EcoR1-Not1 cut cDNA was then ligated into pCSl07 with EcoR1 at the 5' end and Not1 at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 ArgAlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGln 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 AsnSerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspileGluHisHisLeuAla 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                Taylor, R., Zorn, A.M. and Rogers, J. project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence of the control of the collection (XGC) library constructed by Nigel Garrett.

CDNA was oliged Trimed from 5ug of poly A+ RNA from tadpole embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AsnValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GlySerLysLeuLeuIleThrAspArgGlnAspProLeuHisPro--
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89
18
7
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/lab_host="E. coli DH10B"
/clone_lib="XGC-tadpole"
                                                                                                                                                                                                                                                                                                                                                                                                  Hinkton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Kenopus tropicalis EST project 2001
TROPICALIS EXQUENCE ID: TTPA006c03.plkSP6
Sequencing primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                          Silurana tropicalis (western clawed frog) Silurana tropicalis
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/db_xref="taxon:8364"
/clone="TTpA006003"
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Croning,M.D.R., Ashurst,J.L.,
Sanger Xenopus tropicalis EST
Unpublished (2003)
                                                                                                                                     BX705197.1 GI:38367404
                                                                                                                                                                                                                                                             Xenopodinae; Silurana.
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441.50
68.15%
56.69%
23.67%
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Sanger Institute
                                                                                             mRNA sequence.
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                                                                     DEFINITION
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VERSION
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BX705197
LOCUS
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167 SerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPheProSerLeuThrAsnPheLeu 186
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                                                                         127 ValValGlyIleValAspTyrGlyProArgProAsnLysSerGluMetTrpAspValPhe 146
                                                                                                                                                     147 CysTyrArgMetLysAspValAsnCysThr***LysValGlyTyrValGlyAspGlyPhe 166
                                                                                                                                                                                242 TGTTACAGACTGTCAGATGTGTCTGTGTGTGGGAAGTGGGTACGTAGGTAACGGGGAC 301
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                      182 CATGITIGGIATAGIGCIATACAAAGACCCIGIGGACCCCAGCAGCAAATACGACACCITC 241
107 LeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGlnAsnCysGlySerGly 126
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Search completed: April 1, 2004, 13:31:42 Job time: 3253 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:

US-09-466-778B-11

1865

Perfect score:

Sequence:

Total number of hits satisfying chosen parameters:

Listing first 45 summaries

Command line parameters:

Jatabase :

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000

2465228 seqs, 1869859620 residues

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Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

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Sequence 3, Appl:
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TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
FILE REPERENCE: 5820.63
FILE REPERENCE: 5820.63
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR PELICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
PRIOR PLING DATE: 2000-11-02
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
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5 US-10-133-937-18

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7 US-10-023-896-38

4 US-10-023-896-38
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I US-00-044-090-446

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SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 4576
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Alignment Scores:
Pred. No.:
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877.740 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_BUBW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_BUBW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_BUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_BUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
                                                                                                                                             April 1, 2004, 11:22:04; Search time 1504 Seconds
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SUMMARIES

Query Score Match Length DB

No.

Result

Oy 3416 GGGATCTTCTTGCCATCATCGTGACTGGGCTGTTGCCTTGCTTACTCCTAC 3975 Oy 341 PheArgileAsnargivgThrileGlyPhe***HisPhe 353 Db 3976 TTTGGGATAAACGGGAACAATCGGCTTCCAGGATTTT 4014 RESULT 2 US-10-133-112-3 US-10-133-113-112-3 US-10-133-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-112-3 US-10-133-113-113-112-3 US-10-133-113-113-113-112-3	
Score Similarity 95.184	0y 181 SerieuThrashPelreuThrashCanaccacacacacacacacacacacacacacacacacac

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3853 GCAGACGCCAAATGTGTCGACCTCCACTTCCAGGATACCACTGTTGGGGTGTTCCATCTA 3912
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                                                                                                                                                                                                                                                                                                                              LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer 120
                                                                                                                                                                                      ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn
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                                                     AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis
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                                                                                                                       AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu
TITCGGATAAACCGGAGAACAATCGGCTTCCAGCATITT 4791
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APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REFERENCE: 5664.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT APPLICATION NUMBER: US/266,468
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATCHIL VERSION 3.1
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                                                  1802 AGCAAGCTGCTCATCACTGCCAGCCAGGACCCACTCCAACCGAGGGAGACCAGGTTTGTT
                                                                                                                     AlaPheLeuGluHisLeuThrAppLeuSerIleArgGlyThrLeuPheValProGlnAsn
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                                             1755 GCAGACGCCAAAATGTGTCGACCTCCACTTCCAGGATACCACTGTTGGGGTGTTCCATCTA 1814
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                    41 AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
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APPLICANT: Milet, Isabelle
APPLICANT: Milet, Isabelle
APPLICANT: Milet, Isabelle
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
CURRENT APPLICATION UNMER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
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PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
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NAME/KEY: misc_feature
OTHER INFORMATION: Wherein n is A,
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Kekuda, Ramesh
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                                                           APPLICANT: Shimkets, Richard APPLICANT: Patturajan, Meera APPLICANT: Vernet, Corine APPLICANT: Casman, Stacie APPLICANT: Malyankar, Uriel APPLICANT: Shenoy, Suresh
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Zerhusen, Bryan
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Tchernev, Velizar
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Edinger, Shlomit
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Miller, Charles
Boldog, Ferenc
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Best Local Similarity:
Sequence 210, Applica
Publication No. US200
GENERAL INFORMATION:
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1815 GGTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCCAGAGAGGCCTGTGCCAAC 1874
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                                                                                                                                                                 81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100
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                                                                                61 ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn
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41 AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu
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APPLICANT: Patturajan, Meera
APPLICANT: Vernet, Corine
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APPLICANT: Tchernev, Vernet, Corine,
APPLICANT: Zerhusen, Brian
TTIE OF INVENTION: NOVEL MUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CTP
CURRENT PILLING DATE: 2002-03-27
CURRENT PILLING DATE: 2002-03-27
FRICA PAPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR PLICATION NUMBER: 60/262,959
PRIOR PLICATION NUMBER: 60/262,959
PRIOR PLICATION NUMBER: 60/262,959
PRIOR PLICATION NUMBER: 60/212,408
PRIOR PLICATION NUMBER: 60/202,408
PRIOR PLICATION NUMBER: 60/309,99
PRIOR PLILING DATE: 2001-04-20
PRIOR PLILING DATE: 2001-04-20
PRIOR PLILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CURASGELIST VEFEION 0.1
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PEATURE:
NAME/KEY: misc_feature
LOCATION: (3171)..(3171)
OTHER INFORMATION: Wherein n may be a, c,
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Tchernev, Velizar,
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Li, Li,
Liu, Xiaohong,
Malyankar, Uriel,
Miller, Charles,
''ot' Isabelle,
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Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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95.18%
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Rothenberg, Mark,
Sciore, Paul,
                   Kekuda, Ramesh,
Gangolli, Esha,
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LENGTH: 3260
TYPE: DNA
ORGANISM: Homo sapiens
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7860 CTTTCGGATAAACCGGAGAACAATCGGCTTCCAGCATTTT 7899
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Galinger, Shlomit,
APPLICANT: Gangolli, Esha,
APPLICANT: Kekuda, Ramesh,
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Liu, Xiaohong,
Malyankar, Uriel,
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APPLICANT: Sciore, Paul
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Mark
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
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CURRENT APPLICATION NUMBER: US/10/028,248A

CURRENT APPLICATION NUMBER: US/25619

PRIOR APPLICATION NUMBER: 60/256619

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-01-19

PRIOR PILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: 60/272408

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-04-20

PRIOR FILING DATE: 2001-04-20

PRIOR FILING DATE: 2001-07-26

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; LOCATION: (131<u>1</u>)...(1316)
; OTHER INFORMATION: Wherein n is
US-10-028-248A-3
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Edinger, Shlomit
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Smithson, Glennda
                                                             Spytek, Kimberly
Gangolli, Esha
Miller, Charles
    Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
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; NAME/KEY: misc_feature
; LOCATION: (1314)..(1316)
; OTHER INPORMATION: Wherein Xaa may be any naturally occurring amino acid
US-10-107-782-3
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
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LOCATION: (1311)..(1311)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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CURRENT FILING DATE: 2002-03-27
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NAME/KEX: misc feature
LOCATION: (1312).(1312)
OTHER INFORMATION: Wherein n may be a,
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PELLORATION NUMBER: 60/26, 959
PRIOR PELLORATION NUMBER: 60/202, 408
PRIOR PILING DATE: 2001-02-8
PRIOR PILING DATE: 2001-02-8
PRIOR PILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR PELLORATION NUMBER: 60/308, 039
PRIOR PILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311, 266
PRIOR APPLICATION NUMBER: 60/311, 266
PRIOR APPLICATION NUMBER: 60/311, 266
PRIOR APPLICATION NUMBER: 60/311, 266
PRIOR APPLICATION NUMBER: 60/311, 266
PRIOR APPLICATION NUMBER: 60/311, 266
PRIOR APPLICATION NUMBER: 60/309, 344
PRIOR FILING DATE: 2001-03-28
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OTHER INFORMATION: Wherein n may be
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NAME/KEY: misc_feature
LOCATION: (1311). (1311)
OTHER INFORMATION: Wherein n may
                                                                                                                                                                                                                                Taupier, Raymond, jr.,
Tchernev, Velizar,
Vernet, Corine,
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OTHER INFORMATION: Wherein n may
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LOCATION: (1316)..(1316)
OTHER INFORMATION: Wherein n may
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                                       Patturajan, Meera,
Rothenberg, Mark,
Sciore, Paul,
                                                                                                       Shenoy, Suresh,
Shimkets, Richard,
                                                                                                                                               Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
  Charles,
Isabelle,
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THER INFORMATION: Wherein
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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LENGTH: 8495
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7519 GTCAGCATGTTTTTTTACAATGACCTTGTCAATGGCACCACCCTGCAAACGAGGCTGGGA 7578
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                                                                                                                                                                                                                                                                                                                                       8907 ATGACAGGCCCGGGCAAGGCACAAGTGTGAAAAAAGTCACTATGTCGGAGATGGGCTG 6966
                                                                                                                                                                                                                                                                                                                                                                                                                              8967 AACTGTGAGCCGGAGCAGCTGCCCATTGACCGCTGCTTACAGGACAATGGGCAGTGCCAT 7026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7087 CCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCCAGAGAGGCCTGTGCCAAC 7146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7399 GCATTTCTAGAACACCTGACTGACCTGTCCATCCGCGGCACCCTCTTTGTGCCACAGAAC 7458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7459 AGTGGGCTGGGGGAATGAGACCTTGTCTGGGCGGGACATCGAGCACCACGCCAAT 7518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7579 AGCAAGCTGCTCATCACTGCCAGCCAGGACCCACTCCAACCGGTACAAAGTAGGTTTGTT 7638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerAlaArgGlyArg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIle 300
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                                                                                                                                                                                                                                                                                          1 MetThrGlyProGlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeu 20
                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                                                                                                   21 AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis
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                                                                                       8444
296
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                                                                                                                                   Conservative:
Mismatches:
Indels:
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                                                                                         Length:
Matches:
    or
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; OTHER INFORMATION: wherein n is A, US-10-028-248A-1
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1554.00
85.27*
83.85*
83.32*
                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                      Alignment Scores:
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APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
                                                                                                                                                                7800 AGGGATCTTTGCCATCATCCTGGTGACTGGGGCTGTTGCCTTGCCTTACTCCTA 7859
                                                                           7680 TGAIGGAAGAGCCAITCIGCAGIGGGACAICTITGCCICCAAIGGGAICAITCAIGICAI 7739
                                               eSerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly** 320
                                                                                                                                      320 *GlyllePhe******IleIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTy 340
                                                                                                                                                                                                                                                    7860 CITICGGAIAAACCGGAGAACAAICGGCTICCAGCAITIT 7899
                                                                                                                                                                                                                          340 rPheArglleAsnArgLysThrileGlyPhe***HisPhe 353
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CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-02-28
PRIOR PRECIONION NUMBER: 60/285189
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PRILIGATION NUMBER: 60/311266
PRIOR PILING DATE: 2001-07-26
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OTHER INFORMATION: wherein n is A,
                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10028248A Publication No. US20030235882A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taupier Jr, Raymond J
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patturajan, Meera
Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
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Zerhusen, Bryan
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Miller, Charles
Boldog, Ferenc
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Edinger, Shlomit
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LOCATION: (1279)..(1284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 8444
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US-10-028-248A-1
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (166)...(168)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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LOCATION: (163)..(165)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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LOCATION: (1282)..(1284)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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Mismatches:
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NAME/KEY: misc_feature
LOCATION: (1284)..(1284)
OTHER INFORMATION: Wherein n may be a,
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (164)
OTHER INFORMATION: Wherein n may be a,
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LOCATION: (1667..(166)
OTHER INFORMATION: Wherein n may be a,
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LOCATION: (167)..(167)
OTHER INFORMATION: Wherein n may be a,
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NAME/KEY: misc feature
LOCATION: (168). (168).
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LOCATION: (1279)..(1279)
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NAME/KEY: misc_feature
LOCATION: (1280). (1280)
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LOCATION: (1283)..(1283)
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Query Match:
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APPLICANT: Taupier, Maria,
APPLICANT: Taupier, Maria,
APPLICANT: Taupier, Mayond, jr.,
APPLICANT: Taupier, Mayond, jr.,
APPLICANT: Verret, Corine,
APPLICANT: Verret, Corine,
APPLICANT: Struce, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REPERBREE: 21002-23-27
FURBENT APPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PAPLICATION NUMBER: 60/266,619
PRIOR PAPLICATION NUMBER: 60/266,619
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285,189
PRIOR PLING DATE: 2001-04-20
PRIOR PLING DATE: 2001-04-20
PRIOR PLING DATE: 2001-07-26
PRIOR PLING DATE: 2001-07-26
PRIOR PLING DATE: 2001-07-26
PRIOR PLING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/219,344
PRIOR PLING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/219,344
                              7699 TCCAGGCCTTTAAAAGCACCCCTGCCCCGTGACCTTGACCCACACTGGGTGGACA 7758
                                                                                                                                 7759 GGGATCTTTTTGCATCATCCTGGTGACTGGGGCTGTTGCCTTGGCTGCTTACTCCTAC 7818
                                                                                   321 GlyilePhe*****ileIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr 340
  301 SerArg***LeulysAlaProProAlaProValThrLeu***HisThrGlyLeuGly*** 320
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                                                                                                                                                                             341 PheArgileAsnArgLysThrileGlyPhe***HisPhe 353
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 1
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Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Rothenberg, Mark,
Sciore, Paul,
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NAME/KEY: misc feature
LOCATION: (163)..(163)
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (1)..(8025)
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                                                                        APPLICANT: Weigel, Paul
TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
FILE REFERENCE: 5820.6031
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR PLING DATE: 2000-11.02
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin version 3.1
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Mismatches:
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Matches:
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Gaps:
; Sequence 1, Application US/09842930A; Publication No. US20020197681A1; GENERAL INFORMATION:
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1514.50
87.54%
79.32%
81.21%
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Query Match:
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3802 AGCCAACTGCTCATTACCTTCAGCCAGGACCAGCTCCAC---CAAGAGACCAGGTTTGTG 3858
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|TCTGAACCTTTGAGAGCTCCTCCCAGGAGCAACGGCTGCCCACTCTGGGCACTGGGGACA 3978
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3202 CGCTCCCCACTGGGCCAGTACAAACTGACATTTGACAAAGCCAAAGAAGCCTGTGCCAAA 3261
                                                                                                                                                                                            GAAGCTGCGACCATAGCCACCTACAACCAGCTCTCCTATGCCCAGAAGGCCAAGTATCAC 3321
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2775 GCCAACTICTCCACCTICTATGGGATGCTATTGGGCTATGCCAATGCCACCCAGCGGGGT 2834
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   180 ProSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGly 199
                                                                           200 ArgAlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGln 219
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| Publication Wo. US20030003555A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: 90 Human Secreted Proteins
| TILE REFERENCE: P2013P1
| CURRENT APPLICATION NUMBER: US/09/774,639
| CURRENT FILING DATE: 2001-07-09
| PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
| NUMBER OF SEQ ID NOS: 371
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 12
| LENGTH: 2753
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US-09-774-639-12
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Mismatches:
Indels:
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NAME/KEY: misc feature
LOCATION: (7). (7)
CTHER INFORMATION: n equals a,t,g,
FRATURE:
NAME/KEY: misc feature
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US-10-264-237-1320
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SOFTWARE: Patentin Ver. 3.1
LENGTH: 3681
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661.50
53.44%
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                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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; TYPE: DNA; ORGANISM: Homo sapiens
US-09-969-730-13
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                                                                                                                                                                  384 TCAGATGCCATGTGMACTGACCTGCACTTCCAGGAGAAACGGGCTGGCGTTTTCCACCTC 443
                                                                                                                                                                                                                                                                                                                                               81 GlualaalaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLy8AlaLy8TyrHis 100
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                                                      22 Cys---GluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis 40
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APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFENCE: PZ013P2
CURRENT APPLICATION NUMBER: US/09/969,730
CURRENT FILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-02-01
PRIOR PLLING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
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PRIOR PLING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 06/056,731
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
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PRIOR APPLICATION NUMBER: 60/056,366
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PRIOR PEL
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APPLICATION NUMBER: 60/238,291
FILING DATE: 2000-10-06
APPLICATION NUMBER: 09/244,112
FILING DATE: 1999-02-04
Sequence 13, Application US/09969730 Publication No. US20030054443A1 GENERAL INFORMATION:
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Db 1161 ATCCATGCTCTGGCCCCCCTCTGGCACCCCCACAGCCCCAGGCAGTGTGGCGCCT 1220 Qy 314***HisThrGlyLeuGly***GlyIlePhe*****IleIleLeuVal 329	nanan ezz	PRIOR FILING DATE: 1999-02-04 PRIOR FILING DATE: 1999-02-04 PRIOR FILING DATE: 1999-02-04 PRIOR FILING DATE: 1999-02-04 PRIOR FILING DATE: 1998-08-04 PRIOR FILING DATE: 1998-08-05 PRIOR PAPLICATION NUMBER: 60/056,371 PRIOR APPLICATION NUMBER: 60/056,371 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19 PRIOR PELING DATE: 1997-08-19	Detentin Veri 13 2753 A Homo Bapier 3-13 ores: 3 larity: 5 imilarity: 5 imilarity: 5 imilarity: 1	Qy 2 ThrGlyProGlyLysHisLysCysGluCysLysSerHisTyvValGlyAspGlyLeuAsn 21
Alignment Scores: Pred. No.: Bred. No.: 645.50 Matches: 143 Score: 645.50 Matches: 143 Percent Similarity: 22.89\$ Mismatches: 150 Query Match: 10 Gaps: 17 US-09-466-778B-11 (1-353) x US-09-969-730-13 (1-2753) Qy 2 ThrGlyProGlyLy8HisLy8Cy8GluCy8Ly8SerHisTyrValGlyAspGlyLeuAsn 21 21 Qy 2 ThrGlyProGlyLy8HisLy8Cy8GluCy8Ly8SerHisTyrValGlyAspGlyLeuAsn 21 24 AccGCCCGAACACGCGCGTGAACACGCGCGTGAGGGCGTACGGCGTAACACGCGAGGCGATAGACTAGGACGAGGCGAGGCGAGGCAGGGCAGGGCAGGGCGAGGCAGGCAGGGCAGGCAGGCAGGCAGGGCAGGGCAGGGCAG	22 CysGlubroGluGlnLeubrolleAsphrgCysleuGlnAspAsnGlyGlnCysHis	OY 101 LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer 120	180 ProSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGly :::	Qy 260 GlySerLysLeuLeulleThrAspArgGlnAspProLeuHisProThrGlu 276

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InaspasnGlyGlnCysHis 40
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Wrapper or PALM.
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1263 gergéságcaerragerragragócagagerererakeeredérgecegaggekágeee 1322
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                                                                                                       81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100
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                                                                144 CAGGCCACCAGCGGCCCTTATGGTCTGAACTTTTCGGAGGCTGAGGCGGCGATGCGAAGCA 503
384 TCAGATGCCATGTGMACTGACCTGCACTTCCAGGAGAACGGGCTGGCGTTTTCCACCTC 443
                                   61 ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn 80
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804 GCCAACTICTCCACCTICTAIGGGAIGCTAITGGGCTAIGCCAATGCCACCCAGGGGGI
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1323 ATGGGCTTT 1331
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Search completed: April 1, 2004, 14:03:06 Job time: 1541 secs

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Sequence

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Sequence Sequence

Perfect score:

Run on:

Sequence:

Scoring table:

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Sequence :
Patent No.
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                            US-09-1448-545-111

US-09-724-864-28

US-09-902-724-864-20

US-09-902-734-200

US-09-902-735A-200

US-09-902-735A-200

US-09-902-738-200

US-09-818-33

US-09-055-59-35

US-09-055-59-35

US-09-055-59-35

US-09-61468-35

US-09-565-59-36

US-09-565-59-36

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US-09-565-59-36
                                  US-09-010-147B-19
US-08-010-078A-2
US-08-61-218-2
PCT-US94-00253-2
US-09-225-477B-2
PCT-US95-04353-2
US-09-148-545-53
5180808-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 230, Application US/09016434; Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (650) 855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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CLASSIFICATION:
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US-09-016-434-230
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-LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100 -THR MIN-60 -ALIGN=15
-UOSF=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100 -THR MIN-60 -ALIGN=15
-UOSF=45 -DOCALIGN=200 -THR SCORES=00 -MINLEN-0 -MAXLEN-200000000
-USER=USO9466778 @CGN 1 1 69 @runat 01042004 095643 10608 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG $GORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPOX=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOX=10 -XGAPOX=6 -ICPU=6
-FGAPOXT=7 -YGAPOP=10 -YGAPOX=0.5 -FGAPOP=6
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Sequence 212, Appl
Sequence 212, Appl
Sequence 212, Appl
Sequence 125, Appl
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Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
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1 MTGPGKHKCECKSHYVGDGL.....ALAAVSYFRINRKTIGFXHF 353
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                                                                                           1, 2004, 09:56:50 ; Search time 121 Seconds
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   OM protein - nucleic search, using frame_plus_p2n model
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US-08-024-868-1

US-08-242-091-1

US-09-206-695-1

US-09-799-118-1

US-09-494-212

US-09-905-125A-212

US-09-905-125A-212

US-09-905-125A-212

US-09-905-125A-212

US-09-905-125A-212

US-09-905-125A-212

US-09-802-775A-212

US-09-802-775A-212

US-09-802-775A-212

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US-09-802-775A-212

US-08-225-4718-1
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                 US-09-466-778B-11
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Match Length DB
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Database :

1, Appli 35, Appl 35, Appl 35, Appl 35, Appl 35, Appl 6, Appl 6, Appl 6, Appl

Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

853,

Sequence Sequence

Sequence Sequence

Sequence

Sequence

Sequence

Sequence Sequence

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960 GCAGGCGTGGGGGCT------GTGCTTGCCGCTGGAGCATGGC 1001
                                                                                                                               840 AGCCGTATCATTGTGTGGGGACATCATGGCCTTCAATGGCATCATGCTCTGGCCAGC 899
                                                                                                                                                                                      303 ***LeulysAlaProProAlaProValThrLeu------------***His 315
                                                                                                                                                                                                                            900 CCCCTCCTGGCACCCCCAGCCCCAGGCAGCCAGCTGCTGGCGCCTGAAGCCCCACCTGTGGCG 959
                         ----GlnAspProLeuHisProThrGluThrArgCysValAspGly 282
                                                             780 AGTGACGCAGGCCCTGACAACAGTTCCTGGGCCCCTGTGGCCCCCAGGGACAGTTGTGGTT 839
                                                                                                     283 ArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIleSerArg 302
                                                                                                                                                                                                                                                                    316 ThrGlyLeuGly***GlyIlePhe*****IleIleLeuValThrGlyAlaVal----
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                                                                                                                                                                                                                                                                                                                                                 334 AlaLeuAlaAlaTyrSerTyrPheArgIleAsnArgLysThrIleGlyPhe 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lie, Tae Ho
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Wishiewski, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA
TITLE OF INVENTION: Coding Therefor and Uses Thereof
NUMBER OF SEQUENCES: 2
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/642,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/024,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Browdy and Neimark
1: 419 Seventh Street, NW
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-024-868-1; Sequence 1, Application US/08024868; Patent No. 5386013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Livnat, Shmuel REGISTRATION NUMBER: 33,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: VII TELECOMMUNICATION INFORMATION: TELEPHONE: 212-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1414 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-73-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE: Fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
                         266 ThrAspArg---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 69..899
OTHER INFORMATION:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 LeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGlnAsnCysGlySerGly 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 ValvalGlyIleValAspTyrGlyProArgProAsnLysSerGluMetTrpAspValPhe 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 CysTyrArgMetLysAspValAsnCysThr***LysValGlyTyrValGlyAspGlyPhe 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 Ser---TyrSerGlyAsnLeuLeuGlnValLeuMetSerPheProSerLeuThrAsnPhe 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 LeuThrGluValLeuAlaTyrSerAsnSerAraArgGlyArgAlaPheLeuGluHis 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsnSerGlyLeuGlyGlu 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 chdgardargactcacgraraagacacricitcgrccrgrcaargaaggcrrrgrgac 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 AsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsnValSerMetPhePhe 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 TyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGlySerLysLeuLeulle 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 723 GCCAAC---GCCAGCCAGGGGAAGTTGCTTCCGGCCCACTCAGGCCTCAGCCTCATCATCATC 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GACCTGCACTTCCAGGAGAACGGGCTGGCGTTTTCCACCTCCAGGCCACCAGCGGCGCCT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 ThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHisLeuCysSerAlaGlyTrp 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 AppLeuHisPheGlnAspThrThrValGlyValPheHisLeuArgSerProLeuGlyGln 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 TyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsnGluAlaAlaThrMetAla 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LeuProlleAspArgCysLeuGlnAspAsnGlyGlnCysHisAlaAspAlaLysCysVal 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LysCysGluCysLysSerHisTyrvalGlyAspGlyLeuAsnCys---GluProGluGln 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 CGGGTGGGCATAGTCAGCCTGGGTGCCCGCAAGAACCTCTCAGAACGCTGGGATGCCTAC
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143
48
145
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                    Length:
Matches:
TELBFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 230
SEQUENCE CHARACTERISTICS:
LENGTH: 1482 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  7.79e-73
632.50
53.50%
40.06%
33.91%
                                                                                                                                                                 LIBRARY: SPLNNOT04
CLONE: 1561663
                                                                                                                        TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                             Percent Similarity:
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162 GAACGAGCAGCCGGTGTGTACCACAGAGAAGCACGGTCTGGCAAATACAAGCTCACCTAC 221
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APPLICANT: Misniewski, Hans Georg
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5846763
GENERAL INFORMATION:
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266.50
47.42%
32.99%
14.29%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                   Best Local Similarity:
                                                                                              Percent Similarity:
                                       Alignment Scores:
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US-08-024-868-1
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DB:
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190 ----LeuAlaTyrSerAsnSerSerAlaArgGlyArgAlaPheLeuGluHisLeuThrAs 208
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BLICATION NUMBER: US/08/242,097
FILING DATE: 13-WAY-1994
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Matches:
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TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
                                                                                                                                  25,618
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1144 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGEY L.
REGISTRATION NUMBER: 25,
REFERENCE/DOCKET NUMBER:
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47.42%
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CELL TYPE: Fibroblast
CELL LINE: FS-4
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                       linear
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                                                           FILING DATE: 13
CLASSIFICATION:
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LOCATION:
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Oy 72 AspLysAlaArgGluAlaCysAlaAsnGluAlaAlaThrMetAlaThrTyrAsnGlnLeu 91	Db 282 GAGGCAGCCAGAAAATTGGATTCATGTCTGTGCTGCTGGATGGA	152 ASPVALASNCYSThr***LygValGlyTyrValGlyAspGlyPhe	Oy 208 pLeuSerIleArgGlyThrLeuPhevalProCardGGTTTGGGGAAGATACTGGGAAGATACTGGGAAGATACTGGGAAGATACTGGGAAGATGGGAAGATGGGAAGATGGGAAGATGGTGGGAAGATGGTGAGGAAGATGGTGAGGAAGATGGTGAGGAAGATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGTGAGGAAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAGAATGGAAGATGAGAATGGAAGATGAGAATGGAAGAA	SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PILING DATE: 06-Mar-2001 CLASSIFICATION: «Unknown> PRIOR APPLICATION: «Unknown> PRIOR APPLICATION DATA: APPLICATION DATA: ATTORNEY AGENT INFORMATION: ATTORNEY AGENT INFORMATION: REGISTRATION NUMBER: 25,618 REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B TELECOMMUNICATION INFORMATION: TELEPHONE: 212-737-3528 INFORMATION FOR SEQ ID NO: 1:
Db 642 TATGTTGAAATATATGACAGTTACGATGATGTCCATGGCTTTGTGGGAAGATACTGTGGA 701 Qy 208 pleuSexileArgGlyThrLeuPheValProGlnAsnSer 221 :::: :::	RESULT 4 US-09-206-695-1 ; Sequence 1, Application US/09206695 ; Patent No. 6210905 ; GENERAL INFORMATION: ; APPLICANT: Lee, Tae Ho ; APPLICANT: Wishlawski, Hans Georg ; APPLICANT: Vilcek, Jan ; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding		PRIOR APPLICATION: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: FILING DATE: 1994 ATTORNEY/AGENT INFORMATION: NAME: BROWNIN, ROGET L. REGISTRATION NUMBER: LEEZ6/VILCEK=1B TELECHOMUNICATION NIPORMATION: TELECHOMUNICATION NIPORMATION: TELECHOMUNICATION NIPORMATION: TELECHOMUNICATION NIPORMATION: TELECHOMUNICATION NIPORMATION: TELECHOMUNICATION NIPORMATION: TELECHOME: 212-628-5197 TELECHOME: 212-737-3528 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHRACTERISTICS: LENGTH: 1414 base pairs SEQUENCE caid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE: ORGANISM: Homo sapiens CELL LINE: FS-4 FRATURE: NAME/KEY: CDS LOCATION: 69.699 OTHER INFORMATION:	US-09-206-695-1 Alignment Scores: Pred. No.: 26.50 Matches: 64 Score: 26.50 Conservative: 28 Best Local Similarity: 32.99\$ Mismatches: 24 DB: 3.29\$ Indels: 24 CS-09-466-778B-11 (1-353) x US-09-206-695-1 (1-1414) QY 52 ASPThrThrValGlyValPheHisLeuArgSerProLeuGlyGlnTyrLysLeuThrPhe 71 :: Db 162 GAACGAGCAGCGGTGTACCACAGAGAAGCACGTCTGGCAAATACAAGCTCACCTAC 221

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92 SerTyr***GlnLysAlaLysTyrHisLeuCysSerAlaGlyTrpLeuGluThrGlyArg 111
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-466-778B-11 (1-353) x US-09-799-118-1 (1-1414)
                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63, Application US/09484970B
Patent No. 6426186
APPLICANT: JONES, Karen A.
                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
CELL TYPE: Fibroblast
CELL LINE: FS-4
                  LENGTH: 1414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       9.99e-25
266.50
47.42%
32.99%
                                                                                                                                                                                                                                       LOCATION: 69.899
OTHER INFORMATION:
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                                                                                                                                                                                                                    NAME/KEY: CDS
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Best Local Similarit
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                                                                                                                                                                                                 FEATURE
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; LOCATION: 1444, 1455, 1457, 1461, 1463, 1465, 1467, 1497, 1500, 1506, 1521, 1534-; OTHER INFORMATION: a, t, c, g, or other US-09-484-970B-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerTyr***GlnLysAlaLysTyrHisLeuCysSerAlaGlyTrpLeuGluThrGlyArg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ValAlaTyrProThrAla-PheAlaSerGlnAsnCysGlySerGlyValValGlyIleVa 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 lAspTyrGlyProArgProAsnLysSerGluMetTrpAspValPheCysTyrArgMetLy 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 AspThrThrValGlyValPheHisLeuArgSerProLeuGlyGlnTyrLysLeuThrPhe 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AsplysAlaArgGluAlaCysAlaAsnGluAlaAlaThrMetAlaThrTyrAsnGlnLeu 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----beuAlaTyrSerAsnSerSerAlaArgGlyArgAlaPheLeuGluHisLeuThrA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GlnValLeuMetSerPheProSer-LeuThrAsnPheLeuThrGluVal-----
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64
28
78
25
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OTHER INFORMATĪON: Incyte ID No. 6426186 201752.1
NAME/KEY: unsure
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Mismatches:
Indels:
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    APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT APPLICATION NUMBER: US/09/484,970B
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SEQ ID NO 63
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                   3.92e-23
255.50
47.18%
32.82%
13.70%
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
Volkmuth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                            LENGTH: 1734
APPLICANT:
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US-09-907-794A-212 ; Sequence 212, Application US/09907794A

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1028 CGCTGCGACGCTGGCTGGCTGGCAGATG------GCAGCGTCCGCTACCCTGTGGTT 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 TrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGlyTyrVal 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 uAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsnValSerMetPhePh 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 hrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIleSerArg***LeuL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGlnAsnCysGly 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            803 GCCCCAGGCCTGCCACCTGGCGTGCGAAGCTACGGCCCCCCACCGCCGCCTGCACCGC 862
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                                                                                                                                                                                                                                      5 GlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeuAsnCysGluPro 24
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                                                                                                                                                                                         US-09-466-778B-11 (1-353) x US-09-907-794A-212 (1-1985)
                                           Matches:
Conservative:
Mismatches:
Indels:
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            8.42e-16
200.50
35.71%
23.08%
                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Alignment Scores:
Pred. No.:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Mather, Jennie P.
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                                           Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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CORGANISM: Homo sapiens
US-09-907-794A-212
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305 ysAlaproproAlaProValThrLeu***HisThrGlyLeuGly***GlyllePhe---- 323
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PPLICANT: Roy, Margaret Ann

PPLICANT: Stewart, Innothy A.

PPLICANT: Stewart, Daniel

PPLICANT: Williams, D. Mickey

PPLICANT: Williams, P. Mickey

ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145, 222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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CURRENT APPLICATION NUMBER: US/09/905,125A
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                        Sequence 212, Application US/09905125A Patent No. 6664376 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Abhkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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                                1166 TGCTACCGCCAGCA
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US-09-905-125A-212
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968 GATGCCACGATCGCCAAGGTGGACAGCTCTTTGCCGCCTGGAAGTTCCATGGCCTGGAC 1027
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743 GGCIGGCIGCAGGAIGCIACGGIGCAGIACCCCAICAIGIIGCCCCGGCAGCCCIGCGGI
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Indels:
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Matches:
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ 1D NOS: 423
SEQ 1D NO 212
LENGTH: 1985
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23.08%
10.75%
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US-09-905-125A-212
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Query Match:
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1079 CACCCGCATCCTAACTGTGGGC------CCCCAGAGCCTGGGGTCCGAAGCTTTGGC 1129
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CURRENT FILING DATE: 1090-07-10

PRIOR PAPLICATION NUMBER: PCT/USO0/04414

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594
                                                                                   eTyrAsnAspieuValAsnGlyThrThrLeuGlnThrArgieuGlySer-LysLeuLeuI 265
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225 uAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsnValSerMetPhePh 245
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Grimaldi, Christopher J.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Tumas, Daniel
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|1262 GCCATTTT 1269
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Paoni, Nicl
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524 GGGCGTTACCGCTGTGAG------GTCATTGACGGCTGGAGGATGAA--- 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 CTGGTGGAGCTGGAGCTGCGGGGTGTG-----GTCTTTCCTTACCAGTCCCCAAC 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeuAsnCysGluPro 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 GluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHisAlaAspAlaLys 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 CysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeuArgSerProLeu 64
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLING DATE: 1999-11-39
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
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PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
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35.71%
23.08%
10.75%
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US-09-902-775A-212
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Best Local Similarity:
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LENGTH: 1985
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Best Local Similarity: 52.24\$ Mismatches: 23 Query Match: 1 10.64\$ Indels: 1 10.64\$ Indels: 1 10.64\$ Caps: 1	22 CysGlubroGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis	Db 329 ACTGATGCTTTGTGCACTACATTTCCAGGAAAACAGGCTGGTGTCTTCCACATC 388 Qy 61 ArgSerProLeuGlyGlnTyr 67 1::::: Db 389 CAGGCCACCAGTGGCCCTTAT 409 RESULT 11 US-08-225-477B-1	Sequence 1, April Callon US/082294//B Setent No. 5635370 GENERAL INFORMATION: APPLICANT: Susan Hockfield APPLICANT: Diane M. Jaworski TITLE OF INVENTION: BEHAB, A Brain Hya- TITLE OF FUNDENTION: 1 Inronan-Binding Protein NUMBER OF SEQUENCES: 11	ESS nge ord	COUNTRY: C1 COUNTRY: United States ZIP: 06905 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette COMPUTER: IBM PC COMPUTER: MS DOS SOFTWARE: Word Processor		Alignment Scores: 2.45e-10 Length: 1520 Pred. No.: 2.45e-10 Matches: 46 Score: 157.50 Matches: 46 Percent Similarity: 41.21\$ Conservative: 22 Best Local Similarity: 27.88\$ Mismatches: 60
Qy 163 GlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPheProSerLeu 182 Db 883	908 TACCTGGAGCACCTGAGAAGCTGACGCTGACAGAGGCAAGGAGGCCTGCCAGGAAGAT 213GlyThrLeuPheVal-ProGlnAsnSerGlyLeuGlyGl 968 GATGCCACGATGGCCAAGGTGGGACAGCTCTTTGCCGCCTGGAAGTTCCATGGCCTGGAC	Qy 225 uAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsnValSerMetPheph 245	Qy 265 leThrAspArgGlnAspProLeuHisProThrGluThrArgCysValAspGlyArgAspT 285 ::	Qy 305 ysAlaProProAlaProValThrLeu***HisThrGlyLeuGly***GlyllePhe 323 	Qy 324******IlelleLeuValThrGlyAlaValAlaLeuAlaAlaTyrS 339 Db 1202 GCGCATTCCCTCACTGGCTGTATTTATTGAGTGGTTTCCCTTGTGGGTTGGA 1261 Qy 339 erTyrPhe 341 Db 1262 GCGATTT 1269	RESULT 10 US-09-833-381-1252 # Sequence 1252, Application US/09833381 # Sequence 1252, Application US/09833381 # Settent No. 6672186 # GENERAL INFORMATION, # APPLICANT RObienon, Keith E. # TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs # FILE REFERENCE: 5800-119 # CURRENT APPLICATION NUMBER: US/09/833,381 # CURRENT FILING DATE: 2000-02-29 # PRIOR APPLICATION NUMBER: 09/516,448 # PRIOR APPLICATION NUMBER: 09/516,448 # PRIOR PILING DATE: 2000-02-29 # NUMBER OF SEQ ID NOS: 2050 # SOFTWARE: FastSEQ for Windows Version 3.0 # SOFTWARE: FastSEQ for Windows Version 3.0 # STATURE: # NAME/KEY: misc_feature # NAME/KEY: misc_feature # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409) # COATION: (1)(409)	Alignment Scores: 1.12e-16 Length: 409 Pred. No.: 198.50 Matches: 35 Score: 64.18% Conservative: 8

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1174
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                                                                                                                                                                                                                                                                                                                                                                                                   -------AAGYACTGTTCCTAGGTGCCCCTCCCGGC-----AAGCTGACG 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 ArgValAlaTyrProThrAlaPheAlaSerGlnAsnCysGlySerGlyValValGlyIle 130
                                                                                                                                --- LysSerGluMetTrpAsp 144
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                                                                                                        GluCysLysSerHisTyrValGlyAspGlyLeuAsnCysGluProGluGlnLeuProIle 29
                                                                                                                                                                                                                                                                         ------AsnGlyGlnCysHisAlaAspAlaLysCysValAspLeuHisPhe
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                                                              US-09-466-778B-11 (1-353) x US-08-225-477B-1 (1-1520)
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CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9504353
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diana M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: Luronan-Binding Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
Indels:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
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                                                                                                                                                                                       30 AspArgCysLeuGlnAsp-----
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APPLICATION NUMBER: 08/225,47
FILING DATE: APril 8, 1994
ATTORNEY/AGENT INFORMATION:
NAME: MARY M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 1751
TELECOMMUNICATION INFORMATION:
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1295 GTCTACTGCTTCCGA 1309
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  8.45%
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  Query Match:
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971 CCTGATGATCTCTACGATGTCTACTGTTATGCCGAA------GACCTAAAT--- 1015
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1055 TGGGAGGAGGTCGGGACTACTGTCTGGAACGCGGTGCTCAGATCGCTAGCACGGGCCAG 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: RACH, Uwe
APPLICANT: ARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                   DESCRIPTION: DNA encoding a protein
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08340428B; Patent No. 5648465; GENERAL INFORMATION:
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              TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                            157.50
41.21%
27.88%
                                                                                          nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                NAME/KEY: rat BEHAB
                                                                        1520 bases
                                                                                                                                   linear
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                                                                                          TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                   MOLECULE TYPE:
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Best Local Similari
TELEPHONE:
                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                    779 GGTGTCCGGAGCTACGGG---AGACGCGACCCGCAGGAACTCTACGATGTCTACTGCTTT 835
112 ValAlaTyrProThrAlaPheAlaSerGlnAsnCys-----GlySerGlyValVal 128
                                                                                         129 GlylleValAspTyrGlyProArgProAsnLysSerGluMetTrpAspValPheCysTyr 148
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: RACH, Uwe
APPLICANT: NARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 48
                                                                                                                                                                          149 ArgMetLysAspValAsnCysThr***LysValGlyTyrValGly 163
                                                                                                                                                                                                                         836 GCCCGCGAG-----CTAGGGGGTGAAGTCTTTTACGTGGGC 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07306
FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-466-778B-11 (1-353) x PCT-US93-07306-1 (1-5191)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Margolis=1A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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PRIOR APPLICATION DATA: BPLICATION NUMBER: US 07/922,911

FILING DATE: 03-AUG-1992

ATTOMNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9307306 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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44.00%
29.71%
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STRANDEDNESS: single
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ADDRESSEE: Browdy an
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CITY: Washington
STATE: D.C.
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U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LysSerHisTyrVal 16
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                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 NO. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 AUGUST 1992
CLASSIFICATION: 514
ATTORNEY/AGRNT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFRAX: 202-737-3528
                  ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
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TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
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77..3847
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Best Local Similarity:
Query Match:
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539 GAAGTGACGGCGTCGTGTTCCATTATCGGGCGCCCGGGACCGCTATGCGTTGACCTTC 598
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                                                                                                                                                                                                                                                                                                                 92 SerTyr***GlnLysAlaLysTyrHisLeuCysSerAlaGlyTrpLeuGluThrGlyArg 111
                                                                                                                                                                                                                                                                                                                                                      ValAlaTyrProThrAlaPheAlaSerGlnAsnCys------GlySerGlyValVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                        129 GlyIleValAspTyrGlyProArgProAsnLysSerGluMetTrpAspValPheCysTyr 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CAGGACCTGGTAACCCTG 538
                                                                          33 ---LeuGlnAspAsnGlyGlnCysHisAlaAspAlaLysCysValAspLeuHisPheGln 51
                                                                                                                                                                                                                                     72 AsplysAlaArgGluAlaCysAlaAsnGluAlaAlaThrMetAlaThrTyrAsnGlnLeu 91
                                                                                                                                                        52 AspThrThrValGlyValPheHisLeuArgSerProLeuGlyGlnTyrLysLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 ArgMetLysAspValAsnCysThr***LysValGlyTyrValGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           836 GCCCGCGAG-----CTAGGGGGTGAAGTCTTTTÁCGTGGC 871
17 GlyAspGlyLeuAsnCysGluProGluGlnLeuProIleAspArgCys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9503747
GENERAL INFORMATION:
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CAURRINT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION UNBER: 37,643
REFERENCE/DOCKET NUMBER: FP-LJ 1453
TELEPOMUNICATION INFORMATION:
TELEPHONE: (619) 535-8040
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                   506 GGTATCGAGGATGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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112..2848
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STATE: California
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LOCATION:

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997 GGTGGCCTGGACCGCTGCACTCTGGCTGTCTGATGGCAGTGTGCGCTACCCCATC 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                          883 GAGCTGTTCCTGGGTGCCCCT-----CCAGACAAGCTGACCTTGGAGGAGGCGGGACA 936
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                                                                                                                                                                         10 GluCysLysSerHisTyrValGlyAspGlyLeuAsnCysGluProGluGlnLeuProIle
                                                                                                                                                                                                                                                                                                                                                                                       57 ValPheHisLeuArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGlu
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                                                                                                                                                                                                                                                  -----LeuGlnAspAsnGlyGlnCysHis
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             3259
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                                                Conservative:
Mismatches:
Indels:
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                                   Matches:
                Length:
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Job time : 132 secs
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                                          Percent Similarity:
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                       Human ORF
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                                                                                                                                                                                                                                                  Human cDN
                                                                                                                              NOV3 codi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP; proliferative condition; metastasis; inflammation; ischemia; blost defence dysfunction; immune surveillance dysfunction; arthritis; multiple sclerosis; autoimmunity; immune dysfunction; allergy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a human hyaluronan-binding protein, designated BM-HABP.
                                                                                Aaa57362 I
Adb47730 N
Adb63670 F
Aca55632 F
Aaf87114 N
Adb62456 F
Aaf87119 N
                                                                                                                                                                Aaf87117 N
Ach45565 H
Abx74436 H
Abx63446 H
Ade25720 H
Acc72678 H
                                                                                                                                                                                                                                                                                                                                Abv95472 R
Ab168341 R
Abk83989 R
                                   Aaf87113 |
Ab190758 |
Acf04000 |
                                                                                                                                                                                                                                      Abx76382 1
Abx63445 1
Aaq27190
Aav71778
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/transl_except= (pos: 1249. 1251, aa: Xaa)
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Abx76383
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                                                                              AAA57362
ADB47730
ADB63670
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AAF87117
ACH45565
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ADE25720
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ABX63445
AAQ27190
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ABS70406
ABV95472
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ABX76383
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AAI58121
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                       AAC76373
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Abx13823 cDNA enco
Abc08489 Human nov
Agf87120 NOV9 codi
Abc08488 Human nov
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Abc08487 Human nov
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                                                                                                                                                   1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                       OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                             3373863 seqs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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1099 TCCAGGYCTTAAAAAGCACCCCCTGCCCCCGTGACCTTGNCCCACACTGGNTTGGGAGNA 1158
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                                                                                                                                                                                                                                                                                                                                                                                  281 AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisVallle 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HARE, Hyaluronic Acid Receptor for Endocytosis, hyaluronan, chondroitin, chondroitin sulphate, extracellular matrix, cartilage, skin, vitreous humour, endocytic receptor, glycosaminoglycan, human, ss.
               TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro
                                                                                                                                                                                                                     AGTGGGCTGGGGAGAATGAGACCTTGTCTGGGCGGGGACATCGAGCACCACCTCGCCAAT
                                                                                                                                                                                                                                                                            GTCAGCATGTTTTTTTTACAATGACCTTGTCAATGGCACCACCCCGCAAACGAAGGGGTGGGA
                                      TATGTGGGGAGATGGCTTCTCATACAGTGGGAACCTGCTGCTGCTGCTGTCTTCCCCC
                                                                         SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg
                                                                                                      739 TCACTCACAAACTTCCTGACGGAAGTGCTGGCCTATTCCAACAGCTCAGCTCGAGGCCGT
                                                                                                                                                                 GCATTTCTAGAACACCTGACCTGTCCTCTCCGCGGCACCCTCTTTGTNCCACAGAAC
                                                                                                                                                                                                                                                          ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly
                                                                                                                                                                                                                                                                                                                    SerLysLeuLeuIleThrAspArgGlnAspProLeuHisProThrGluThrArgCysVal
                                                                                                                                                                                                                                                                                                                                                979 AGCAAGCTGCTCATCACTGACAGACAGACCCACTCCACCGGACGAGGACCAGGTGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                             1039 GATGGAAGAGACACTCTGGAGTGGGACATCTGTGCCTCCAATGGGATCACACATGTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                          SerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.
                                                                                                                                  AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn
                                                                                                                                                                                                 SerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn
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/note= "No start codon given"
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                                                                                                                                                                                                                                         New hyaluron-binding proteins, known as full-length WF-HABP, WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 Argacaggecegggeaagcacaagrgrgagrgraaagrcacrargreggagargggerg 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, arthritis, multiple sclerosis, autoimmunity, immune
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Mismatches:
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(AMNA-) AMERICAN NAT
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Best Local Similarity:
Query Match:
DB:
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WO200039166-A1
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                                                         20-DEC-1999;
                                                                                      23-DEC-1998;
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3496 TCACTCACAAACTTCCTGACGGAAGTGCTGGCCTATTCCAACAGCTCAGGTCGAGGCCGT 3555
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                                                                                        201 AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn 220
  SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 SerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly*** 320
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                                                                                                                                                                                221 SerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn
                                                                                                                            3556 GCATTICTAGAACACCTGACTGACTGACCATCGCGGCACCCTCTTTGTGCCACAGAAC
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                                                                                                                                                                                                                                                                        ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly
                                                                                                                                                                                                                                                                                                                      3676 GTCAGCATGTTTTTCTACAATGACCTTGTCAATGGCACCACCCTGCAAACGAGGCTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGly1leThrHisValIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Hyaluronan receptor for endocytosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3976 TITCGGATAAACCGGAGAACAATCGGCTTCCAGCATTTT 4014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "No start codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3256 CTGTGCTCAGCAGGCTGGCTGGAGACGGGGGGGGTTGCCTACCCCACAGGCTTCGCCTCC 3315
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                                                                                                                                                                                                                                                                                                                                         The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAMA7675 and AAM47684). HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroltin (C) or chondroltin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is the coding sequence for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2956 ATGACAGGCCCGGGCAAGCACAAGTGTGAAGTGTAAAAGTCACTATGTCGGAGATGGGCTG 3015
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                                                                                                                                                                                              New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetThrGlyProGlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeu
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                                                                                                                                                                                                                                                                                                Claim 49; Fig 33; 263pp; English.
                                                                                          Weigel JA;
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1772.00
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                                                                                        Weigel PA, Zhou B,
                                                                                                                                   WPI; 2002-049271/06
(WEIG/) WEIGEL P A. (ZHOU/) ZHOU B. (WEIG/) WEIGEL J A.
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Best Local Similarity:
                                                                                                                                                           P-PSDB; AAM47684
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                                                                                                                                                                                                 The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) teceptor for endocytosis (HARE) or a cell that does not express functionally active HARE. The method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing increaction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing metastasis by preventing interaction between tumour cells having HARE on its surface. The second method is useful for preventing materiasis by preventing interaction between tumour cells having HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This sequence encodes the human 190kba Hyaluronan cells expressing (HARE)
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                                                                      Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of by using hyaluronan, HARE, and/or monoclonal antibody that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4642 BP; 1141 Å; 1215 C; 1216 G; 1070 T; 0 U; 0 Other;
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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express tunctionally active HARE. The method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing meteastasis by preventing interaction between tumour cells having HA, CD or CDS coat and con-tumour cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This sequence encodes a longer version of the human coal having a response the number of the human and the coal having a response the number of the human and the coal having a response the number of the human and the coal having the presence of HA, CD and CDS for the coal that the coal that the number of the human are coal that the coal that the coal that the coal that the number of the human are coal that the coal that the number of the human are coal that the coal that the coal that the coal that the coal that the number of the human are coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that the coal that t
                                                                                                                                                                                                                                                                                                   Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of by using hyaluronan, HARE, and/or monoclonal antibody that binds to
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                                                                                                               Weigel PH, Weigel JA;
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(WEIG/) WEIGEL P H. (WEIG/) WEIGEL J A.
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Sequence 4962 BP; 1249 A; 1277 C; 1311 G; 1125 T; 0 U; 0 Other; Conservative: Mismatches: Indels: Matches: Length: 3.08e-193 1772.00 95.18% 94.62% 95.01% Similarity:

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3733 Argacadececedeceaageacaaagrereaagreraaaagreacrararereegagaregeere 3792
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                                   1153 GAAAIGIGGGAIGICIIICIGCIAICGGAIGAAGAIGIGAACIGCACCIGCAAGGIGGGC 4212
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141 GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic; nootropic; antidepressant; immunosuppressive; antibacterial; antiparasitic; virucide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
                                                                                                                                                                                                                         AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4633 TCCAGGCCTTTAAAAGCACCCCCTGCCCCCGTGACCTTGACCCACACTGGGAGCA
                                                                                                              4213 TATGTGGGAGATGGCTTCTCATGCAGTGGGAACCTGCTGCTGCAGGTCCTGATGTCCTTCC
                                                                                                                                                SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg
                                                                                                                                                                                     1273 TCACTCACAAACTTCCTGACGGAAGTGCTGGCCTATTCCAACAGCTCAGCTCGAGGCCGT
                                                                                                                                                                                                                                                              4333 GCATTICIAGAACACCIGACIGACCIGICCAICCACGGGGCACCCICTIIGIGCCACAGAAC
                                                                                                                                                                                                                                                                                                                                       4393 AGTGGGCTGGGGGAGAATGAGACCTTGTCTGGGCGGGACATCGAGCACCACCACCTCGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 SerLysLeuLeuIleThrAspArgGlnAspProLeuHisProThrGluThrArgCysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4693 GGGATCTTCCCATCATCCTGGTGACTGGGGCTGTTGCCTTGGCTGCTTACTCCTAC
                                                                         TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro
                                                                                                                                                                                                                                                                                                      SerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn
                                                                                                                                                                                                                                                                                                                                                                             ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly
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replace(1034,T)
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                                                                                                                                                                                                                                                                                                                                                                New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of several novel human proteins, designated NOVX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, palsy, epilepsy, Lesch-Whan syndrome, Multiple sclerosis, talsy, Lesch-Whan syndrome, multiple sclerosis, darsay telanguectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autolimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              graft-versus-host disease. The present sequence is a coding sequence of
                                                                                                                                                                                                                            Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U; Shenoy S, Spytek KA, Gangolli B, Miller C, Boldog F, Li L; Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD; Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3260 BP; 774 A; 886 C; 850 G; 749 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Page 24-25; 363pp; English.
                                                                                                      2001US-0262959P.
2001US-0272408P.
2001US-0285189P.
                                                                                      2000US-0256619P
                                                                                                                                                 26-JUL-2001; 2001US-0308039P.
09-AUG-2001; 2001US-0311266P.
                                                         19-DEC-2001; 2001WO-US050076
                                                                                                                                                                                                                                                                                                                                                                                                              or Alzheimer's disease.
                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                    2002-666903/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
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WO200259315-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                        Rothenberg M;
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                                                                                                        19-JAN-2001;
                                                                                                                   28-FEB-2001;
                                                                                                                                   20-APR-2001;
                                                                                        19-DEC-2000;
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                            01-AUG-2002
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2234
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1875 GAAGCTGCGACCATGGCAACCTACAACCTAGCTCTCCTATGCCCAGAAGGCCAAGTACCAC 1934
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                                                                                                                                                                                                                                                                                                                                                                                     TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro 180
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                                                                                                                                                                                                                      CAGAACTGTGGCTCTGGGTTTGGGATAGTGGACTATGGACCTAGACCAACAAGAGT
                                                                                                                                                                                                                                                                          141 GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn
                                                    101 LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer
                                                                                                                                                                  121 GlnAsnCysGlySerGlyValValGlyIleValAspTyrGlyProArgProAsnLysSer
                                                                                                                                                                                                                                                                                                                              2055 GARATGTGGGATGTCTTCTGCTATCGGATGAAGATGTGAACTGCACCTGCAAGGTGGGC
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therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
                                                                                                                                               Vernet C, Fernandes
     NOV11; NOV12; NOV13; NOV14; NOV15; ds
                                                                                                                                                                                                      Claim 9; Page 32-33; 141pp; English.
                               Location/Qualifiers 387. .2024
                                                  /product= "NOV9"
                                                                                                                                              Shimkets RA, Lichenstein H,
                                                                                                  19-NOV-1999; 99US-0166336P.
29-NOV-1999; 99US-0167985P.
08-MAR-2000; 2000US-0187944P.
16-NOV-2000; 2000US-00715417.
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immune disorders.
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                                                             WO200136638-A2
                   Unidentified
                                                                          25-MAY-2001
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This sequence encodes the NOV9 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic convictions, and their coding sequences. The proteins have Cytostatic contrivities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient, sequence NOVX or proteins, by inserting the muclaic acid into a cell and culturing it to patients own production of protein. They are used to produce NOVX or proteins, by inserting the muclaic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, and which carriers may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated contracting the serime/threonine kinase. Il phosphorylation sites characteristic of serime/threonine kinase. Il phosphorylation altes characteristic of serime/threonine kinase. CC e.g. Peutz-Jeghers syndomen callular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) -1 ke super family and are involved in, e.g. regulation of cell cevelopment, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat canders. Inflammatory disorders, immune disorders, inflammatory disorders, immune disease e.g. hypertrophic cardiovasc Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and

Sequence 3625 BP; 896 A; 971 C; 914 G; 844 T; 0 U; 0 Other;

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New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, crohn's disease, atherosclerosis, cancer, Huntington's disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of several novel human proteins, designated NOVX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, Von Hippellindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epliepsy, Lesch-Whan syndrome, multiple sclerosis, ataxia telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The present sequence is a coding sequence of
                                                                                                                                                                                                                                                  Human, NOVX, single nucleotide polymorphism, SNP, anti-HIV, cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic; nootropic; antidepressant; immunosuppressive; antibacterial; antiparsitic; virucide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U, Shenoy S, Syptek KA, Gangolli E, Miller C, Boldog F, Li Li, Taupier RJ, Kekuda R, Santibson G, Zerhusen BD, Liu X, Colman SD; Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
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                                                                                                                                                                                                               Human novel protein NOV1b coding sequence SEQ ID NO: 3.
CTITCGGATAAACCGGAGAACAATCGGCTTCCAGCATTTT 3029
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                                                                                               ВР
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28-FEB-2001; 2001US-02072408P.
20-APR-2001; 2001US-0208189P.
26-JUL-2001; 2001US-0308039P.
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P-PSDB; ABJ10587.
                                                                                               ABT08488 standard;
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                                                                                                                                      ABT08488;
                      2990
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Length: Matches:

3.39e-168 1558.00

Alignment Scores: Pred. No.:

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6948 ATGACAGGCCCGGGCAAGCACAAGTGTGAGTGTAAAAGTCACTATGTCGGAGATGGGCTG 7007
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137
   Conservative:
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Indels:
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                                                                                    US-09-466-778B-11 (1-353) x ABT08488 (1-8495)
85.31%
84.75%
83.54%
 Percent Similarity:
Best Local Similarity:
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7800 AGGGAICTICTITGCCAICAICCTGGIGACTGGGGCTGIIGCCTIGGCTGCTIACTCCTA 7859
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                                                                                                                                                                                                                                           Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory; hypotensive; neuroprotective; anorectic; nootropic; antidepressant; immunosuppressaive; antibacterial; antiparasitic; virucide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antinfertility; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of several novel human proteins, designated NOVX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ian M, Vernet CAM, Casman SJ, Malyankar U;
Gangolli E, Miller C, Boldog F, Li L;
Smithson G, Zerhusen BD, Liu X, Colman SD;
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                                                                                                                                                                                                              Human novel protein NOV1a coding sequence SEQ ID NO: 1.
                                                        7860 CTTTCGGATAAACCGGAGAACAATCGGCTTCCAGCATTTT 7899
                            340 rPheArglleAsnArgLysThrIleGlyPhe***HisPhe
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                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Shenoy S, Spytek KA, Gangolli
Taupier RJ, Kekuda R, Smithson
Tchernev V, Si J, Edinger S,
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2001US-0262959P.
2001US-0272408P.
2001US-0285189P.
2001US-0308039P.
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26-JUL-2001;
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hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia telangiectasia, leukodystrophes, addiction, anxiety, depression, pain, obesity, cron's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmne disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parastic infections, or graft-versus-host disease. The present sequence is a coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7147 GAAGCIGCGACCAIGGCAACCIACAACCAGCICICCIAIGCCCAGAAGGCCAAGTACCAC
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                                                                                                                                                                                                                                           Sequence 8444 BP; 2251 A; 2105 C; 2147 G; 1929 T; 0 U; 12 Other;
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                                                                                                                                      GlyilePhe*****ileIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAM47675 and AAM47684). HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in
                                                                                                                                                                                                                                                                                                                                    HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; vitreous humour; endocytic receptor; glycosaminoglycan; rat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related nucleic acid.
                         AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIle
          SerlysleuleulleThrAspArgGlnAspProLeuHisProThrGluThrArgCysVal
                                                                                                                                                                                                                                                                                                                Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence
                                                                                                                                                                                              7819 TITCGGATAAACCGGAGAACAATCGGCTACCAGCATITT 7857
                                                                                                                                                                                   341 PheArgileAsnArgLysThrIleGlyPhe***HisPhe 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                'product= "Rat HARE"
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is the coding sequence for rat HARE
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GATGGAAGATCCATTCTGCAGTGGGACATCATCGCCGCCAATGGAATCCTCCATATTATT 3918
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                                            SerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly*** 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express functionally active HARE. The method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemcherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least
                                                                                                                                                                                                                                                                                                                                                                                  Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; rat; gene; ss.
                                                                                                         Gly1lePhe*****1le11eLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr
                                                                                                                                                                                                                                                                                                                                                     cDNA encoding rat 175kDa Hyaluronan receptor for endocytosis (HARE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "HARE"
/note= "Hyaluronan receptor for endocytosis"
PheArglleAsnArgLysThrIleGlyPhe***HisPhe 353
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Location/Qualifiers
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P-PSDB; ABG72498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on presenting accertaints second method is useful for preventing metatlesis by preventing interaction between tumour cells having HA, CD or CDS coat and non-tumour cells expressing HARE on its surface. The invention also a biological fund for detecting the presence of HA, CD and CDS in receptor for endocytosis (HARE)
                                                                                                                                                                                                                                                                                                                                                                                                                3022 ATGACGGGCCCAGGCAAGCATAAGTGTAAAAGTCACTATGTCGGGGACGGAGTG 3081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, open reading frame, ORFX, detection, cytostatic, hepatotropic, vulnerary; antipsoriatic, antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiatchritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianamatory; antianaemic; gene therapy; cancer; proliferative antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; choesternol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                     3979 GGTATATTCTGTGCCGTCGTCCTGGTCACTGGTGCGATTGCTCTGGCAGCTTACTCTTAC
                                                  AspGlyArgAspThrieuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIle
                                                                     3859 GATGGAAGATCCATTCTGCAGGGACATCATCGCCGCCAATGGAATCCTCCATATTATT
                                                                                                                  SerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide sequence SEQ ID NO:3855.
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05-APR-1999;
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             anticonvulent; antiathritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; dermatological; immunosuppressive; antithromatic; antithromatic; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiavascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPheProSer 181
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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ATGTGGGATGTCTTCTGCTATCGGATGAAGATGTGAACTGCACCTGCAAGGTGGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuThrAsnPheleuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 rlysleuteulleThrAspArgGlnAspProLeu--HisProThrGluThrArgCysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 CAAGCTGCTCATCACTGCCAGCCCAGCACCACTNNCCAACCGACGGAGCCAGGTTTGTT
                                                                                                                                                                                                                                                                                                                                                enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1377 BP; 303 A; 398 C; 342 G; 330 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
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Query Match:
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;

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This sequence encodes the NOV2 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX
                                                                       340
 SerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly*** 320
                      724 GGGATCTTCTTTGCCATCATCCTGGTGACTGGGGCTGTTGCCTTGGCTGCTTACTCCTAC 783
                                                                                                                                                                                                                                                                                                                                                                                         NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiowyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV9; NOV10; NOV11; NOV12; NOV14; NOV15; NOV16; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                     GlyIlePhe******IleIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr
                                                                                                                                           PheArglleAsnArgLysThrIleGlyPhe***HisPhe 353
                                                                                                                                                                               TTTCGGATAAACCGGAGAACAATCGGCTTCCAGCATTTT 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 10-13; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "NOV2"
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99US-0167785P.
2000US-0187844P.
                                                                                                                                                                                                                                                   AAF87113 standard; DNA; 2011
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                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                             NOV2 coding sequence.
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29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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AAF87113
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proteins, by inserting the nucleic acid into a cell and culturing it to detect and quantizate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in aspatient for an antigens in the production of antibodies (Abs) against NOVX and in aspats to identify modulators of NOVX expression and activity. The anti-NOVX Abs are used for down regulate expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treaded vary depending on the NOVX protein. NOVI, NOVI, NOVI, NOVI, 100 NOVI and NOVI and are used for teat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception) NOV2-1 NOVS and NOVS are homologous to the epidermal growth factor (BGF) cles meaning the protein management, and are used to treat cancers, and motility and protein management, and are used to treat cancers, immune disorders and cellular adhesion disorders of inflammatory disorders, immune disorders and cellular adhesion disorders and motility and stellular proliferations and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders and cardiovascular disease e.g. hypertrophic cardiowapopathy, long-OT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1549 GAAGCTGCGACCATGGCAACCTACAACCAGCTCTCTATGCCCAGAAGGCCAAGTACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1609 CTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGGTTGCCTACCCCACAGCCTTCGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 yTyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 oSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2011 BP; 458 A; 551 C; 583 G; 419 T; 0 U; 0 Other;
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Mismatches:
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84.87%
84.87%
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1801 IGCATTICTAGAACACCTGACTGACTGTCCATCCGCGGCACCCTTTTGTGCCCACAGAA 1860
                                                                                                                 1861 CAGTGGGCTGGGGGAGAATGAGACCTTGTCTGGGCGGGACATCGAACACCACCTCGCAA 1920
                                                                                                                                                                                              1921 TGTCAGCATGTTTTTCTACAATGACCTTGTCAATGGCACCACCCTGCAAACGAGGCTGGG 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antiacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
200 gAlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                            220 nSerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAs
                                                                                                                                                        240 nValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 1320; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                1981 AAGCAAGCTGCTCATCACTGCCAGCCAGGAC 2011
                                                                                                                                                                                                                                     260 ySerLysLeulleThrAspArgGlnAsp 270
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multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

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2235 ACCGGCCTGAACACACGGCGCTGTGAGTGCCACGCAGGCTACGTAGGCGATGGACTGCAG 2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGGAGCCGTCCTTGCTTCCCTCAGCTCTCTGCTGCCCAGCAGCTGGGCTTCCAC 2534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 AsnSerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAla 239
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                                               Sequence 3681 BP; 648 A; 1172 C; 1123 G; 731 T; 0 U; 7 Other;
from WIPO at ftp.wipo.int/pub/published_pct_sequences
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145
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Conservative:
Mismatches:
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3132 ATCCATGCTCTGGCCAGCCCCCTCCTGGCACCCCACAGCCCCAGGCAGTGCTGGCGCCT 3191
                                                                                                                                                                 3234 GCTGGAGCACTGCTTGGCTTGGTTGGCCGGAGCTCTCTACCTCCGTGCCCGAGGCAAGCCC 3293
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lymphatic endothelial glycoprotein; CLEVER-1; inflammation; common lymphatic endothelial and vascular endothelial receptor 1; antiinflammatory; dermatological; antiinflammatory intimetalogical; antiinflammatory intiasthmatic; cytostatic; hepatotropic; antiarteriosclerotic; nootropic; immunosuppressive; skin inflammation; acute inflammatory disease; chronic inflammatory disease; chronic inflammatory disease; diabetes; connective tissue disease; chronic inflammatory sease; diabetes; lung disease; asthma; adult respiratory district; osteoarthritis; lung disease; asthma; adult respiratory distress syndrome; sarcoidosis; ulcerative colitis; Crohn's disease; non-viral hepatitis; cirrhosis; cholagitis; atherosclerosis; vasculitis; thyroiditis; multiple sclerosis; myositis; ischaemia reperfusion injury; transplantation rejection;
                                                                       ***HisThrGlyLeuGly***GlyIlePhe*****IleIleLeuVal 329
                                                                                                                                          330 ThrGlyAlaVal-----AlaLeuAlaAlaTyrSerTyrPheArgIleAsnArgLysThr 347
297 ThrHisVallleSerArg***LeuLysAlaProProAlaProValThrLeu----- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New purified lymphatic endothelial glycoprotein, designated as common lymphatic endothelial and vascular endothelial receptor- (CLEVER-1), recognizable by a monoclonal antibody, useful for treating inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "CLEVER-1"
/note= "common lymphatic endothelial and vascular
endothelial receptor 1"
                                                                                                        3192 GAAGCCCCACCTGTGGCGCCAGGCGTGGGGGCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CLEVER-1 encoding cDNA SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                        ACF04000 standard; cDNA; 7879 BP.
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The present sequence encodes a human lymphatic endothelial glycoprotein, designated as common lymphatic endothelial and vascular endothelial receptor a scommon lymphatic endothelial and vascular endothelial receptor 1 (CLEVER-1). Which has a molecular weight of 270-300 kD in sodiuw dodecyl sulphate-polyacrylande gel electrophoresis (SDS-PAGE) cunder non-reducing conditions, recognisable by a monoclonal antibody constraint the group consisting of DSM ACC 2519 or 2590. Also described: (1) a CLEVER-1 antibody; (2) a cell-free preparation comprising CLEVER-1; (3) diagnosing inflammatory diseases in a patient; (4) detecting malignant cells in a patient; (5) identifying an agent that stimulates or inhibits the binding of CLEVER-1 to cells; (6) removing malignant cells from a sample; (7) treating inflammation in a patient; (8) preventing metastasis in a patient; and (9) stimulating CLEVER-1; (8) preventing metastasis in a patient; and (9) stimulating CLEVER-1; contidiated; antirheumatic, antiarthritic, osteopathic, antiasthmatic, antidiabetic, antiartheumatic, not cupacity, instrumentory contropic and contropic and the present invention can be used for treating inflammation; diabetes, or chronic inflammatory diseases so from a setting inflammation; diabetes, or chronic inflammatory diseases sond as skin inflammation; diabetes, osteoarthritis), obstructive and restrictive lung diseases (such as ulcerathritis), ties and Crohn's diseases, varial diseases (such as theroselize path and path of path of path of path of path of path of path of path of path of path of path of path of path of path of path of path of path of path of p
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1027 GCCAACTICTCCACCTICTAIGGGAIGCIATIGGGCTAIGCCAALGCCACCCAGCGGGT
                                                                                                                                                                 AsnValSerMetPhePyrAsnAspLeuValAsnGlyThrLeuGlnThrArgLeu
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                      180 ProSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGly
                                                                                                                                                                                                                                                                                                         297 ThrHisVallleSerArg***LeuLysAlaProProAlaProValThrLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WF-HABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a human hyaluronan-binding protein, designated
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/transl except= (pos: 1255. 1257, aa: Xaa)
/transl except= (pos: 1297. 1299, aa: Xaa)
/note= "Xaa is an unspecified amino acid"
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                                                                                                                                                                                                                                                                          New hyaluron-binding proteins, known as full-length WF-HABP, WF-HABP, HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OB-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, arthritis, multiple sclerosis, autoimmunity, immune
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35.208
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                                                                                                                                      Liau G,
                                                    HUMAN GENOME
AMERICAN NAT
                                                                                                                                                                                              WPI; 2000-452376/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                              P-PSDB; AAY93911.
23-DEC-1998;
                                                                                                                                      Hastings GA,
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985 CCAGGGACAGTTGTGGTTAGCCGTATCATTGTGTGGGACATCATGGCCTTCAATGGCATC 1044
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| GCTGGAGGCACTGCTTGGCTTGGTGGCCGGAGCTCTCTACCTCCGTGCCCGAGGCAAGCCC 1206
                                                                                                                                                                                                                                                                                                                 277 ThrArgCysValAspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIle 296
                                                                                                                                                                                                                                                                                                                                                                           297 ThrHisValIleSerArg***LeuLyBAlaProProAlaProValThrLeu------ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                           314 -----***HisThrGlyLeuGly***GlyIlePhe*****IleIleLeuVal 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 ThrGlyAlaVal-----AlaLeuAlaAlaTyrSerTyrPheArgIleAsnArgLysThr 347
                                                                                                                      ||| :::::: ||| 868 AACGCCACCCTCCTAAGTGCCAAC---GCCAGCCAGGGAAGTTGCTTCCGGCCCACTCA 924
                                                                                                                                                                                                                                                      260 GlySerLysLeuLeulleThrAspArg-----GlnAspProLeuHisProThrGlu 276
                                                                                                                                                                                                                                                                         200 ArgAlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGln 219
                                                                                  240 AsnValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeu 259
180 ProSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGly 199
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1207 ATGGGCTTT 1215
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Search completed: April 1, 2004, 12:37:58 Job time : 586 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model
Run on: April 1, 2004, 09:56:50 ; Search time 4925 Seconds
(without alignments)
3106.617 Million cell updates/sec
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Title:
US-09-466-778B-11
Perfect score: 1865
Sequence:
1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 7.0
Delop 6.0 , Delext 7.0

Total number of hits satisfying chosen parameters: 694.
Minimum DB seq length: 0000000000
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 044.

3470272 segs, 21671516995 residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Command line parameters:
-WODEL=framet p2n.model -DEV=x1h

Command line parameters:
-MODBL=frame+ p2n.model -DEV=xlh
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-Q=/Cgn2_1/USPTO gpool/US09466778/runat_01042004_095642_10579/app_query.fasta_1.519
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GenEmbl:*

1: 9D_htg:*

2: 9D_htg:*

3: 9D_in:*

4: 9D_on:*

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6: 9D_pat:*

7: 9D_ph:*

11: 9D_ph:*

12: 9D_pr:*

13: 9D_pr:*

14: 9D_pr:*

15: em_bh:*

16: em_hth:*

17: em_hth:*

18: em_hth:*

21: em_or:*

22: em_or:*

23: em_pat:*

24: em_ph:*

25: em_ph:*

27: em_fth:*

em vi:*	em htg hum:*	em_htg_inv:*	em_htg_other:*		em_htg_pln:*			em htg vrt:*	em_sy:*	em htgo hum: *	em_htgo_mus:*	em htgo other:*
29:	30:	31:	32:	33:	34:	35:	36:	37:	38:	39:	40:	41:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

em_un:*

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AY227444

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KAKIISSDIISTNGTVHIIDKLLSPKNLLIPKDNSGRILQNLTTLATINGYIKFSNL
IQDSGLLSVITDPIHTPVTLEMPTDQALHALPABQODFL FNQONKDKLKEYLKFHVIR
DAKVLAVDLPTSTAMKTLQGSEPSLSKOGAGRDIGDLFLNGQTCRIVQRELLFDLGVAY
GIDCHLIDPTLGGGROTPTTPPASGEGGSCVNTPSCPRWSKPKGVKQLYNLFPFRN
LEGGRERCSLVIQIPRCCKGYFGRDCQACPGGPDAPCNNRGVCLDQYSATGECKCNTG
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CSCQKGYKGDGHSCTEIDPCADGLNGGCHEHATCKMTGPGKHKCECKSHYVGDGLNCE
PEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPLGQYKLTFDKAREACANE
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AECTQTGPNQAACNCLPAYTGDGKVCTLIYVCLTKNGGCSEFAICNHTGQVERTCTCK
PNYIGDGFTCRGSIYQELPKNPKTSQYFFQLQEHFVKDLVGPGPFTVFAPLSAAFDEE
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SEMMDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFPSLTNFLTEVLAYSNSSA
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QTRLGSKLLITASQDPLQPTETRFVDGRAILQWDIFASNGIIHVISRPLKAPPAPVTL
                              PRI 23-APR-2003
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                                                                                                                                                                                                                                                                           Zhou, B., McGary, C.T., Weigel, J.A., Saxena, A. and Weigel, P.H. Uurlification and molecular identification of the human hyaluronan receptor for endocytooan dispersion of the human hyaluronan dlycobiology 13 (5), 339-349 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="190 kDa hyaluronan receptor for endocytosis"
/function="mediates endocytosis of hyaluronan or
chondroitin sulfate via the clathrin coated pit pathway"
/note="generated by proteolytic processing of a larger
protein; probably a product of the HARE/Stabilin-2 gene;
190 kDa protein purified from spleen"
                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 4492)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="hyaluronan receptor for endocytosis precursor"
'protein_id="AA039681.1"
'db xref="G1:28848630"
Submitted (29-JAN-2003) Biochemistry and Molecular Biology, University of Oklahoma Health Sciences Center, BMSB Room 860,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISNPLYESTISAPPEPSYDPFIDSEERQLEGNDPLRIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                     AY227444.1 GI:28848629
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Homo sapiens
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KEYWORDS
SOURCE
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AUTHORS
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FEATURES

Alignment Scores:

ORIGIN

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3621
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DLVNGTTLQTRLGSKLLITASQDPLQPTETRFVDGRAILQWDTFASNGIIHVISRPLK
APPAPVTLTHTGLGAGIFFAIILVTGAVALAAYSYFRINRRTIGFQHFESBEDINVAA
LGKQQPENISNPLYESTTSAPPEPSYDPFTDSEERQLEGNDPLRTL"
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NHGGCDKNABCTQTGPRQAANCLPAYTGDGKVCTLINVCTKNGGGESFAICHHTGQ
NBRCTCTCKNYIGDGFTCRGSIYQELPKNPKTSQYFPQLQEHPVKDLYGPGFTVFRAB
LSAAFDEEARVKDWDKYGLMPQVLRYHVVACHQLLLENIKLISNATSLQGEPIVISVS
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GYIKFSNLIQDSGLLSVIIDPIHTPVTLFWPTDQALHALPAEQODFLFNQDNKDKLKE
YLKFHVIRDAKVLAVDLPTSTAWKTLQGSELSVKCGAGRDIGDLFLNGQTCRIVQREL
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REACANBEATWATYNQLSYAQKAKYHLCSAGWLETGRVAFTAFASONGGSGYVGIV
DYGPRPNKSBMPDYFQYRKDVNCTCKYGYVGDGFSCSGNLLQVLAFFPSLTNETEV
LAYSNSGARGRAFLEHLTDLGIRGTLFVPQNGGLGENETLSGRDIEHHLANVSNEFYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Pax:81-438-52-3914)
NEDO human cDNA sequencing project supported by Ministry of
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YNLPFKRNLEGCRERCSLVIQIPRCCKGYFGRDCQACPGGPDAPCNNRGVCLDQYSAT
GECKCNTGFNGTACEMCWPGRFGPDCLPCGCSDHGQCDDGITGSGQCLCETGWTGPSC
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GRCNQGPLGDGSCDCDVGWRGVHCDNATTEDNCNGTCHTSANCLTNSDGTASCKCAAG
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  GlyllePhe******IleIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr 340
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4575)
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The nucleotide sequence of a long cDNA clone isolated from
                                                                                                                                                                                                                                                       AKO24503 4575 bp mRNA linear F
Homo sapiens mRNA for FLJ00112 protein, partial cds.
AKO34503
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                                                                                                  341 PheArgileAsnArgLyBhrileGlyPhe***HisPhe 353
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Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
Direct Submission
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/dev_stage="adult"
/note="vector:pBluescriptII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="FLJ00112 protein"
/protein_id="BAB15793.1"
/db_xref="GI:10440526"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="as00112"
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fis (full insert sequence)
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|gene="FLJ00112"
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LHLAKVDGNIT1EGASIVDGDNAATNGVIHIINKVLVPQRRLTGSLPNLLMRLEQMPD
YSIFROYIOYNLANAIEAADAYTVPRPNNNAIENYTRKYLSLEEDVLRYHYVLEE
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ACETCTEGKYGIHCDQACSCVHGRCNQGPLGDGSCDCDVGWRGVHCDNATTEDNCNGT
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GDGTLCSEMPPCTGLTPGGGSRNAECIKTGTGTHTCVQQGGWTGNGRDCSBINNCLLP
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GVWSCVCQEGYBGGDGFCKGFRGNGIDCEPITSCLEQTGKCHPLASCQSTSS
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                                                                                                                                                                                      3915 GGGATCTTCTTTGCCATCATCCTGGTGACTGGGCTGTTGCCTTGGCTGCTTACTCCTAC 3974
3855 rocaddecriraaaadcaccececececerdacerraaceacacacredocridadada 3914
                                                                                                                                      GlyIlePhe*****IleIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr 340
                                             SerArg***LeuLysAlaProProAlaProValThrLeu***HisThrGlyLeuGly*** 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library construction and clone selection: Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .ya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
nucleotide sequence of a long cDNA clone isolated from human
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Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                     3975 TITCGGATAAACCGGAGAACAATCGGCTTCCAGCAITIT 4013
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/note="vector:pBluescriptII SK plus"
                                                                                                                                                                                                                                         341 PheArgileAsnArgLysThrileGlyPhe***HisPhe
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/product="FLJO0122 protein"
/protein_id="BAB84877.1"
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2 (bases 1 to 5604)
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AK074051
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/clone="FLJ00122"
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/db_xref="taxon:9606"
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fis (full insert sequence).
Homo sapiens (human)
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CHTSANCLTNSDGTASCKCAAGFQGNGTICTAINACEISNGGCSAKADCKRTTFGRRV
CTCKAGYTGOGIVCLEINPCLENHGGOENNAECTOTGPNQAACNCLPAYTGDGKVCTL
INVCLTKNGGGCSEFAICHTGQVERTCTCKPNYIGBGFTCRGSIYQELPKNPKTSQYF
FQLQEHTWYDLWGGFPTVFRELSAAFDEEAAVKWHNKYGLMFQVNXTHVYACHGLLL
ENLKLISNATSLGGEPTVISVSQSTVYINNKAKIISSDIISTNGIVHIIDKLLSPKNL
LITFRONSGRILQWLTTLAINNGYIRFSNLQOBGLESVITDPHTPFWTLFRPFDQAL
HALPABQQDFLFNQDNKDTKEYLKFNYINDAKVLAVDLFTSTAMYTLQGSELSVKCG
AGRDIGDLFLNAQTGRIVGRIVKEYLKFHYINDAKVLAVDLFTSTAMYTLQGSELSVKCG
AGRDIGDLFLNAQTGRIVGRIVGRIVGRIDGSCRESCSLVIGIPTGGROPFTTFPRSGRCG CPGGPDAPCRNRGVCLDQYSATGECKCNTGFNGTACEMCWPGREGPDCLPCGGCSDHGG
CDGTTGSGOCLCETGWTGTSCDTQALLPAVCTPPCSAHATTCKBNNTCECNLDYSEDG
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GRVAYPTAFASQNCSGSVVGTYDYGRPRNSEMWDYFCYRNKDVNCTCKVGYVGDGF
CSGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGB
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Matches: Conservative: Mismatches: Indels: Length: 3.46e-164 1772.00 95.18% 94.62% 95.01% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: .. No

1 MetThrGlyProGlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeu US-09-466-778B-11 (1-353) x AK074051 (1-5604)

3984 ATGACAGGCCCGGGCAAGCACAAGTGTGAGTGTAAAAGTCACTATGTCGGAGATGGGCTG 4043 40 4044 AACTGTGAGCCGGGAGCTGCCCATTGACCGCTGCTTACAGGACAATGGGCCAGTGCCAT 21 AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis ò

4103

4163 9 4104 GCAGACGCAAATGTGTCGACCTCCACTTCCAGGATACCACTGTTGGGGTGTTCCATCTA 41 AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu PP

80 ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn 19 ò

1164 cécréceséreséceserarasécreacerrisacaaseceasassecrereceae

4223

4224 GAAGCTGCGACCATGGCAACCTACAACCTACCTATGCCCTATGCCCCAGAAGGCCAAGTACCAC 4283 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 81 à

101 LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer ò

4284 CTGTGCTCAGCAGGCTGGCTGGAGACCGGGGGTTGCCTACCCCACAGCCTTCGCCTCC 4343 140 g

GlnAsnCysGlySerGlyValValGlyIleValAspTyrGlyProArgProAsnLysSer 4344 CAGAACTGTGGCTCTGGTGGGTTGGGATAGTGGACTATGGACCTAGACCCAACAAGAGT 121 à g

4403

160

4463

4523

141 GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr**LysValGly 4404 GAAATGTGGGATGTCTTCTGCTATCGGATGAAGATGTGAACTGCACCTGCAAGGTGGGC à

TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro 180 4464 TATGTGGGAGATGGCTTCTCATGCAGTGGGAACCTGCTGCAGGTCCTGATGTCCTTCCCC 161 q

SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg

181

201 AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn 220 ò

4524 TCACTCACAAACTTCCTGACGGAAGTGCTGGCCTATTCCAACAGCTCAGCTCGAGGCGGT

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4704 GTCAGCATGTTTTTCTACAATGACCTTGTCAATGGCACCCTGCAAACGAGGCTGGGA 4763
                                                                                                     4644 AGTGGGCTGGGGGAGAATGAGACCTTGTCTGGGCGGGACATCGAGCACCACCTCGCCAAT 4703
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                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-DEC-2000) Hideki Adachi, RIKEN, Cellular Biochemistry Laboratory; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan (E-mail:adachih@postman.riken.go.jp, Tel:81-48-467-9372,
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SCALNLGVKCPDGYTMITSGSVGVRDCRYTFEVRTYSLSLPGCRHICRKDYLQPRCCP
                                                                                                                                                                                                                                                                                                   AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisVallle 300
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FEEL-1, a novel scavenger receptor with in vitro bacteria-binding and angiogenesis-modulating activities
J. Biol. Chem. 277 (37), 34264-34270 (2002)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                           221 SerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn
                                                                                                                                        ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly
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/product="FELE-2"
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TSGGWRGVCDGGYEGDGFLCYGNAAVELSFLSEAA FNRWINNASIQPTLSATSNLT
VLYSFQQATEDMDQDEKSPULSQSNIPALGYTYRHMLGTYRVADLQTLESSDMLATSLQ
GNFLHLAKYDGNITIEGASIVDGDNAATNGYHIINKVLYPQRRLGSSDMLARLEG
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LEEKKLIKNDLHNGMRRETMLGFSYFLSFFLHNDQLYVNEAPINYTNVATDKGVIHGLG KULEIQKARCDNNDTTIIRGRCRTCSSELTCFFGTKELGIBERRRCLTYTSYFWRRTLIF
GGCPKCVRTVITRECCAGFFGPCOPCPGNAONVCFGNGICLDGVNGTGVCGGGF
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KNLLITPKDNSGRILQNITTLATNNGYIKFSNLIQDSGLLSVYTDPHTFFYTLLEWPTT
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Conservative: Mismatches: Indels: Length: Matches: 5.6e-164 1772.00 95.18% 94.62% 95.01% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: No.:

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US-09-466-778B-11 (1-353) x AB052958 (1-8214)

AspGlvLeu 20 3ATGGGCTG 6668	GlnAspAsnGlyGlnCysHis 40	AGGACAATGGGCAGTGCCAT 6728	ValGlyValPheHisLeu 60		golualaCysalaasn 80	
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1 MetThrGlyProGlyLysHisLysCysGluCySLysSerHisTyrValGlyAspGlyLeu 20	21 AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis 40	6669 AACTGTGAGCCGGAGCTGCCCATTGACCGCTGCTTACAGGACAATGGCCAGTGCCAT 6728	41 AlaAspalaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu 60	6729 GCAGACGCCAAATGTTGTGTCGACCTCCACTACCACGATACCACTGTGGGGGGTGTTCCATCTA 6788	61 ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn 80	
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6789 GGCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCCAGAGAGGCCTGTGCCAAC 6848

GluAlaAlaThiMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100

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FEXZ, a novel cell adhesion molecule of Fas-1 superfamily mediates Unpublished
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Direct Submission
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KCGAGRDIGDLFLNGQTCRIVQRELLFDLGVAYGIDCLLIDPTLGGRCDTFTTFDASG
ECGSCVNTPSCPRWSKPKGVKQKCLYNLPFKRNLEGCRERCSLVIQIPRCCKGYFGRD
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DEMPYTLTRSKGEIFNSDKOQIKLKHGGKKKYKTIQGDITANGLHTLDRANDKL
EPPFESNNEQTIMPULDRYSKFRSILEETNLGHALDBDGVGGPYTIEVPNNEALNN
KDGTLDYLLSPEGSRKLLELVRYHIVPFTQLEVATLISTPHIRSMANQLIQFNTTDNG
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VYWGRCPANSEPTALPTHRCVYSGRFGSLKSGCARYCNATVKIPKCCKGFYGPDCNQC
PGGFSNPCSGNGQCADSLGGNGTCICEEGFQGSQCQFCSDPNKYGPRCNKKCLCVHGT
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GYSGOGTLCSEMDPCTGLIPGGCSRNARCIKTGTGTHTCVCYQQANTGNBDCSEINNC
LLPSAGGTIDNASLYVGPGQNECEKKGFRONGIDCEPITSCLEGTGKCHPLASCQS
TSSGVWSCVCQEGYBGDGFLCYGNAAVELSFLSBAAIFNRWINNASLQPTLSATSNLT
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GNFLHLAKVDGNITIEGASIVDGDNAATNGVIHIINKVLVPQRRLTGSLPNLLMRLEQ
MPDYSIFRGYIIQYNLANAIEAADAYTVFAPNNNAIENYIREKKVLSLEEDVLRYHVV
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GDG1TCTVVDFCKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTE1DPCADGLN
GGCHBHATCKWTGPGKHKCECKSHYVGDGLNCEPEQLP1DRCLQDNGQCHADAKCVDL
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SARALQWDTFASNGIIHVISRPLKAPPAPVTLTHTGJGAGIFFAILVYGAVALAAY
SYRRINRTIIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPEPSYDPFTDSE
ERQLEGNDPLRTL
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NANCTTVAPGRTECICQKGYVGDGLTCYGNIMERLRELNTEPRGKWQGRLTSFISLLD
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(31-MAY-2003) Department of Biochemistry, School of Kyungpook National University, 101 Dongin-dong, Jung-gu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="FAS1, EGF-like and X-link domain containing adhesion molecule-2"
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HSA295695 HOMO sapiens mRNA for stabilia A1295695 A1295695.1 GI:18073427 STAB2 gene; stabilin-2. Homo sapiens (human) Homo sapiens Homo sapiens Homo sapiens Turayota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Jummalia; Eutheria; Primates; Johansson, S., Svineng, G., Fratlongati, P., Velten, F. W., Joha Stabilin-1 and -2 constitute Blochem. J. 362 (Pt 1), 155-121818465	Politz, O., Gratchev, A., McCou Guillot, P., Johannson, S., Bir Ganlich, C., Orfanos, C.B., Jo Stabilin-1 and stabilin-2 con domain-containing adhesion mo endothelial-macrophage differ Unpublished 3 (bases I to 8266) Gratchev, A. Direct Submission Submitted (27-JUL-2000) Gratc University Medical Center Man Mannheim, GERMANY Revised by author 27-APR-2001	/ Organism="Homo sapi / mol type="mRNA" / db type="mRNA" / db type="mRNA" / db type="mRNA" / gene="STAB2" / gene="STAB2" / codon start=! / prodon start=! / prodon start=! / prodon="start=! / prodon="start=! / prodon="start=! / prodon="start="start="dela" (201342) / db xref="Gp1:1807342] / db xref="Gp1:1807342] / db xref="Gp1:1807342] / db xref="Gp1:1807342] / db xref="Gp1:1807342] / db xref="SpTREMBL:" / translation="bmRLQHI" / translation="bmRLQHI" / translation="bmRLQHI" / kranslation="bmRLQHI"	SSYONCYMOSCIDGDGG SSYONCYMOSCIDGDGG KLECKCLENYRGDGKYCDPI PVDPCQINFCRACTOFI RAYAMPLSKLGBFTVLLFTI TDMRYTLTGKGGFTNNLDFTI TDMRYTLTGKGGFTNNLDFTI TDMRYTLTGKGGETNNLDFTI TDMRYTLTGKGGETNNLDFTI TDMRYTLTGKGGETNNLDFTI CDGTLDYLLSPEGSTNTLETRK QUILANDVANEEIEITAKUGE VYWSRCPANSEPTALFTRC PGGFSPNCSCONGOADSLGG CNNTIDSDGACLFGTTRC CNNTIDSDGACLFGTTRC CNNTIDSDGACLFGTTRC CNNTIDSDGACLFGTTRG CNNTIDSDGACLFGTTRG CNNTIDSDGACLFGTTRG GYEGDGTLCSEMDPCTGLTI LLESAGGCHANDASCLYOPG TSSGVWSCVCQEGYEGDGFT VLVPSQCATEDMDQDEKSFN GNFHLLAKVDGNITIEGASI MPDYPIFRGYIIQYNLANDAI LEEKLLIKNDLHNGMTRETNIN KVLEIQKNRCDNNATTIIRG
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Johannstitute a novel family of fasciclin molecules associated with erentiation and angiogenic processes
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hansson, S. and Goerdt, S.
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6732 7032 7152 6792 7092 ATGACAGGCCCGGGCAAGCACAAGTGTAAAAGTCACTATGTCGGAGATGGGCTG 6672 7153 TCACTCACAAACTTCCTGACGGAAGTGCTGGCCTATTCCAACAGCTCAGCTCGAGGCCGT 7212 6793 GGCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCCAGAGAGGCCTGTGCCAAC 6852 180 200 LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer 120 GlnAsnCysGlySerGlyValValGlyIleValAspTyrGlyProArgProAsnLysSer 140 GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly 160 40 9 80 MetThrGlyProGlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeu 20 21 AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis ArgSerProLeuGlyGlnTyrLysLeuThrPheAspLysAlaArgGluAlaCysAlaAsn GAAATGTGGGGATGTCTTCTGCTATCGGATGAAAGATGTGAACTGCACCTGCAAGGTGGGC TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro 41 AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu 6733 GCAGACGCCAAATGTCTCGACCTCCAGGATACCACTGTTGGGGTGTTCCATCTA TATGTGGGGAGATGCTTCTCATGCAGTGGGAACCTGCTGCAGGTCCTGATGTCCTTCCCC SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg CAGAACTGTGGCTCTGGTGGGTTGGGATAGTGGACTATGGACCTAGACCCAACAAGAGT 8266 334 2 17 0 Matches: Conservative: Mismatches: Indels: Gaps: Length: US-09-466-778B-11 (1-353) x HSA295695 (1-8266) 5.65e-164 1772.00 95.18% 94.62% 95.01% Percent Similarity: Best Local Similarity: Alignment Scores: 6973 141 7033 7093 Н 6913 121 101 161 181 6613 61 Query Match: DB: Pred. No.: ORIGIN Ω g g gg g P δ ò 8 ö Ωp à à à Db à Š ద à

λō	201	AlaPheLev	GluHisLeuThrA	AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn	ThrLeuPheValP	roglnAsn	7
DP	⊣	GCATTTCTA	AGAACACCTGACTG	ACCTGTCCATCCGCGGC	ACCCICITIGIGC	CACAGAAC	N
& &	221	SerGlyLeu	1G1yG1uAsnG1uT 1GGGGAGAATGAGA	SerClyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn 	IleGluHisHist 	euAlaAsn	240
ð	241	ValSerMet	PhePheTyrAsnA	eppeuValAsnGlyThr	ThrieuGlnThra	rgLeuGly	9
qa	7333	GTCAGCATO		GICAGCATGITITITITITACAATGACCITGICAATGGCACCACCCTGCAAACGAGGCTGGGA	ACCCTGCAAACGA	GGCTGGGA	7392
8 8	261	SerLysLeu	LeulleThraspa	SerlysLeuleulleThrAspArgGlnAspProLeutisProThrGluThrArgCysVal	ProThrGluThrA	rgCysVal	80
gg	7393	AGCAAGCTO	SCTCATCACTGCCA	GCCAGGACCCACTCCAA(CCGACGGAGACCA	GGTTTGTT	7452
ò a	281 7453	AspGlyArc GATGGAAGA	JAspThrLeuGluT ::: \GCCATTCTGCAGT	AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisVallle AttGGAAGACCATTCTGCAGTGGGACATCTTTGCCTCCAATGGGATCATTCAT	AsnGlylleThrH AATGGGATCATTC	isvalile ATGTCATT	300
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λō	341	PheArgile	AsnArgLysThrI	PheArglleAsnArgLysThr11eGlyPhe***HisPhe	353		
DÞ	7633	TTTCGGAL	AACCGGAGAACAA	rceecriceacerir	7671		
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AUTHORS	- O E M G O	himkets, R. alyankar, U oldog, F., erhusen, B.	A., Patturaja J., Shenoy, S., Li, L., Taupie D., Liu, X., C	Shimkets,R.A., Patturajan,M., Vernet,C.A., Casman,S.J., Malyankar,U., Shenoy,S., Spytek,K.A., Gangolli,E., Miller, Boldog,F., Li,L., Taupier,R.J., Kekuda,R., Smithson,G., Carhusen,B.D., Liu,X., Colman,S.D., Toherney,V., Si,J., Ed	Casman, S.J. golli, E., Mil swithson, G.	ler, C., , Edinger	, s
TITLE JOURNAL		uman nucle atent: WO	sic acids and 02059315-A 21	polypeptides and r 0 01-AUG-2002;	verg,m. nethods of us	e thereof	
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λo	Н		/ProGlyLysHisL	MetThrGlyProGlyLysHisLysCysGluCysLysSerHisTyrValGlyAspGlyLeu	HisTyrValGlyA	spGlyLeu	20
da	1635	ATGACAGG	CCGGGCAAGCACA	AGTGTGAGTGTAAAAGT	CACTATGTCGGAG	ATGGGCTG	1694

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LOCUS AF160476 3260 bp mRNA linear PRI 12-JUL-2000
DEFINITION Homo sapiens CD44-like precursor FELL mRNA, complete cds.
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               AsnCysGluProGluGlnLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis
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SNLIODSGLLSVITDP.HHTPVTLKPPPDALHALPARQDPERPRODNOKLKETLKFPH
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SSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNG
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VTLTHTGLGAGIFFAIILVTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQ
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                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3260)
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                                                                                                                                                                                                                                                                                                                                                    Tao,Q., Zhang,W. and Cao,X.
Direct Submission
Submitted (21-JWA-1999) Department of Immunology, Shanghai
Brilliance Biotechnology Institute & Second Military Medical
University, 800 Kiangyin Road, Shanghai 200433, P. R. China
Location/Qualifiers
                                                                                                                                                                                                                  Tao, O., Zhang, W. and Cao, X. Molecular cloning and characterization of human FELL sharing homology with CD44 Unpublished
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171_.2864
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AF160476.1 GI:9049505
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/Organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" Alignment Scores: 2.48e-143 Length: 3625 Fred. No.: 1558 00 Matches: 300 Forcent Similarity: 85.31\$ Conservative: 2 Best Local Similarity: 84.75\$ Mismatches: 15 Cuery Match: 63.54\$ Indels: 37 DB: 03-09-466-778B-11 (1-353) x AX149461 (1-3625)	1 MetThiGlyProGlyLysHisLysCysGl 	0y 21 AsnCyBGluProGluGInLeuProIleAspArgCysLeuGlnAspAsnGlyGlnCysHis 40	Oy 41 AlaAspAlaLysCysValAspLeuHisPheGlnAspThrThrValGlyValPheHisLeu 60	Oy 61 ArgserProLeuGlyGlnTyrLysLeuThrPheAspLysAlaAargGluAlaCysAlaAsn 80	Oy B1 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100	Oy 101 LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrFroThrAlaPheAlaSer 120	Qy 121 GlnAsnCysGlySerGlyValValValGlyIleValAspTyrGlyProArgProArgDroSer 140 Db 2438 CAGAACTGTGGCTCTGGTGTGGGTTAGGATTAGTGGACTATGGACCTAGACCCAACAAGAGT 2497	Qy 141 GluMetTrpAspValPheCysTyrargMet_LysAspValAsnCysThr***LysValG1 160 Db 2498 GAAATGTGGGATGTCTTCTGCTATCGGATGAAAG	Qy 160 yTyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePr 180 Db 2531 2531	Qy 180 oSerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerAlaArgGlyAr 200	0y 200 galabheLeuGluHisLeuThrAspleuSerIleArgGlyThrLeuPheValProGlnAs 220 1 11
	TyrvalGlyAspGlyPheSerTyrSerGlyAsnLeuGlnValLeuMetSerPhePro	Oy 181 SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerAlaArgGlyArg 200	Qy 201 AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn 220	Qy 221 SerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn 240	Qy 241 ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly 260	Oy 261 SerLysLeuleThrAspArgGlnAspBroLeuHisProThrGluThrArgCysVal 280	Qy 281 AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIle 300	Qy 301 SerArg***LeuLysAlaProProAlaProValThrLeu***#19ThrGlyLeuGly*** 320	Qy 321 GlyllePhe******IelleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr 340	Qy 341 PhearglleasnargLysThrIleGlyPhe***Highhe 353	RESULT 9 AX149461 LOCUS DEFINITION Sequence 17 from Patent W00136638. AX149461 DEFINITION Sequence 17 from Patent W00136638. AX149461 AX14

IDYEGDGITCTVUDFCK DGINGGCHEHATCKMTG CVDLHFODTTVGFTRF SAGWLETGRVAFTAFA SSRPEDERFPDDLISTG LQTRLGSKLLITASQDP LTHTGLGAGIFFAIILV NISNPLYESTTSAPPEP DOlyA signal 3574 3579 IN IN INMENT SCOYES:	Pred. No.: 2.49e-143 Length: Score: 1558.00 Matches: Secret: Similarity: 85.31	1 MetThrdlyProGlyLysHisLysCysGluCysLys:		81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSer' 2335 GAAGCTGCGACCATGGCAACCTACAACCAGCTCTCC 101 LeuCysSerAlaGlyTrpLeuGluThrGlyArgVal,		180 OSErLeuThrAsnPheLeuThrGluValLeuAlaTy. 2549
P PORIGIN Alignm	Pred. Score Perce Best Query DB: US-09	o do	60 PB PG PG PG PG PG PG PG PG PG PG PG PG PG	yo da oo	8 8 8 8 8 8	B & B & B & B & B & B & B & B & B & B &
2810 TGATGGAAGAGCCATTCTGCAGTGGACATCTTTGCCTCCAATGGGATCATTCAT		Homo Bapiens (human) M Homo Bapiens (human) Homo Bapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3642) Blum, H. Bauwisachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S. Direct Submission Submitted (15-NOV-1999) MIPS, Am Klopferspitz 18a. D-82152	lar Genome Analy 8. wiemann@dkfz] milians Universi NA sequencing co available at th courcenzentrum, H			/coduce="hypothetical protein" /produce="hypothetical protein" /produce="hypothetical protein" /produce="hypothetical protein" /produce="gen:e453578" /db_xref="gen:e453578" /db_xref="goa.:09UF98" /db_xref="GOA::09UF98" /db_xref="goa.:09UF98" /db_xref="goa.:09UF98" /translation="woravord goar vorteing goar goar goar goar goar goar goar goa
8 6 8 6 8 8	RESULT 10 HSM801377 LOCUS DEFINITION ACCESSION VERSION KERYWORDS	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	COMMENT	FEATURES BOULCE	gene	

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VARCSQKGTKVSCSCQKGYKGDGHSCTEIDPCA
KSHYVGDGINCEPEQLPIDEDCLODNGQCHADAK
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SGYFRINRYTIGFGHFESEEDINVAALGKQOPE
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81 GlualaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr*** 7188 GAAGCTGGGACCATGGCAACCTACAACCAGCTCTCTATGCC 101 LeuCySesrAlaGlyTpLeuGluThrGlyArgValhaTyr 7248 CTGTGCTCAGCAGGCTGGAGACCGGGGGGGTTGCTAC 121 GlnAsnCysGlySerGlyValValGlyTlsValAspTyrGly 7308 CAGAACTGTGGCTCTGGTGGTGTGGGTTAGGAACTATGGAA 141 GluMetTrDAspValPheCysTyrArgMet-LysAspValAs 7368 GAAATGTGGGATCTCTTCTGCTATCGGATGGAAG 160 yTyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGl 7401	Qy 340 rPheArglleAsnArgLysThrIleGlyPhe***HisPhe 353
260 ySettysLeuleullaThrAsphrgGlnAspProleuHisProThtGlThrAgoysy 260 260 ASGAGCTCCTCATCACCCAGGACCACCACCACGACGACGACGACGACGACGAC	#3.54\$ Indels: Gaps: Gaps: 1933) x AX686194 (1-8495) IMPROGLYLYSHISLYSCYSGLUCYSLYSSETI GCCCGGGCAAGCAAGTGTAAAAGT IUPTOGLUGINLEUPFOILEASPARGCYSLEUC IUPTOGLUGINLEUPFOILEASPARGCYSLEUC IUPTOGLAGAGCACCAAGTGTAAAAGT IUPTOGLAGAGCACCCCATTGACCGCTGCTTAAAGT AGCCGGAGCAGCTCCCATTGACCGCTGCTTACACGGATACC FOLEUGINGATTGTCGACTTCAGGATACC TOLEUGINGATAAGCTGACTTCAGGATACC TOLEUGINGATAAGCTGACTTCAGGATACC FOLEUGINGATAAGCTGACTTCAGAGAAAAC TAGAGGGCCAGTATAAGCTGACTTGACAAAAAC TAGAGGGCCAGTATAAGCTGACCTTTGACAAAAAAAAAA

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Submitted (25-AUG-2000) Department of Biochemistry and Molecular Biology, University of Oklahoma Health Sciences Center, 940 Stanton L. Young, BMSB 860, Oklahoma City, OK 73104, USA Location/Qualifiers
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SKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYG
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VEGCQNLCTVVIQTFRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTG
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   SerLysLeuLeulleThrAspArgGlnAspProLeuHisProThrGluThrArgCysVal 280
                                                                                                                      281 AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisVallle 300
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                   Gly1lePhe*****1le1leLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr
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Zhou,B., Weigel,J.A., Saxena,A. and Weigel,P.H.
Molecular Cloning and Functional Expression of the Rat 175-kDa
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Rattus norvegicus hyaluronan receptor for endocytosis HARE
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Mol. Biol. Cell 13 (8), 2853-2868 (2002)
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Zhou, B., Weigel, J.A. and Weigel, P.H.
Direct Submission
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Stone, D., Sciore, P., Millet, I. and Rothenberg, M. Human nucleic acids and polypeptides and methods of use thereof Patent: WO 02059315-A 1 01-AUG-2002; Curagen Corporation (US)
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Mismatches:
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Matches:
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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/db xref="GI:19705589"
/translation="MARSKLLIGKLLPLILIFLGLLVQNACSPTEAPELTKRCDKKST
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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    ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly
                                                                                                                                                                  SerLysLeuLeulleThrAspArgGlnAspProLeuHisProThrGluThrArgCysVal
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Guillot,P., Johansson,S., Svineng,G., Franke,P., Kannicht,C.,
Kzhyshkowska,J., Longati,P., Velten,F.W., Johannson,S. and
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Biochem. J. 362 (Pt 1), 155-164 (2002)
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Mus musculus stabilin-2 mRNA, complete cds.
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/mol_type="mRNA"
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/tissue_type="liver"
62. .7741
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RGQAFLKHLTDISIRGTLFVPQNSGLFGNKSLISGRDIEHHLTNVNVSTYNDLVNGTFL
RTMLGSQLLITPSQDQLHQFTRFVDGRSILQMDIIAANGILHISEPLRAPPTAATAA
HSGLGTGIFCANVYTYGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSMLLASSSPRIS
QTLCMRPQRRHPQSPPVTPSQTLENRIWRTATLWGHCGPDMRSQQATTVTVPR"
                                  VCTPACSVHATCTENNTCVCNINYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVS
CSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCE
PEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHIRSPLGQYKLTFDKAKEACAKE
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    /product="hyaluronan receptor for endocytosis HARE"
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QEDGQVCLPUDECOTES TOTAL SLITTLE EQMPPYS ISPRCY I HYNLASA I BAADAYTVEVPNNEA I ESYTREKKATSLKE
DILQYHVVLGEKLIRNDLHNGHREFNLGFSYLLAFFLHNDQLYVNEA PINTNVATD
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Matches:
Conservative:
Mismatches:
Indels: (1-8157)Gaps: US-09-466-778B-11 (1-353) x AF364951 6.89e-136 1487.00 86.978 77.908 79.738 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 61 . No. : Score: à 음 8 g δ g ò 셤

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81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100

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7168 7288 7345 7405 6928 7048 7108 6811 200 220 7228 08-JUN-2001 280 GlyIlePhe******IleIleLeuValThrGlyAlaValAlaLeuAlaAlaTyrSerTyr 340 GlnAsnCysGlySerGlyValValGlyIleValAspTyrGlyProArgProAsnLysSer 140 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 7346 GATGGAAGACCATTCTGCAGTGGGACATCATTGCCTCTAACGGGGTTCTCCATATCATT Serarg***LeuLysalaProProAlaProValThrLeu***HisThrGlyLeuGly*** 7466 GGCATATICTGCGCTGTCGTCCTGGTTACTGGTGCGATTGCTCTGGCTGCCTACTCCTAC 6989 TACGIGGGCGAIGGCTICTCCTGCAAIGGGAACCIGCTGCAGGTCCTCAIGTCCTICCC SerLeuThrAsnPheLeuThrGluValLeuAlaTyrSerAsnSerSerAlaArgGlyArg AlaPheLeuGluHisLeuThrAspLeuSerIleArgGlyThrLeuPheValProGlnAsn SerGlyLeuGlyGluAsnGluThrLeuSerGlyArgAspIleGluHisHisLeuAlaAsn GTCAACGTCTCCTTTTACGATGACCTTGTCAATGGTACCGTCCTGAAGACTAGGCTGGGA Asccaachechcancaccasccassachcascrocac---caasassccassrrcsrs AspGlyArgAspThrLeuGluTrpAspIleCysAlaSerAsnGlyIleThrHisValIle 7406 TCTGAACCTTTGAAAGCTCCTCCCACGCCGCAACGGCTGCCCACTCTGGCCTAGGAACA LeuCysSerAlaGlyTrpLeuGluThrGlyArgValAlaTyrProThrAlaPheAlaSer CTCTGCTCAGCTGGCTGGCTGGAGAGAGGGGGGTTGCCTACCCCACGATCTACGCCTCT GluMetTrpAspValPheCysTyrArgMetLysAspValAsnCysThr***LysValGly TyrValGlyAspGlyPheSerTyrSerGlyAsnLeuLeuGlnValLeuMetSerPhePro eceriririonanchecricacticacerecenteneracececereriristicaceaeane ValSerMetPhePheTyrAsnAspLeuValAsnGlyThrThrLeuGlnThrArgLeuGly SerLysLeuLeulleThrAspArgGlnAspProLeuHisProThrGluThrArgCysVal Shinkets, R.A., Lichenstein, H., Vernet, C. and Fernandes, E. Polypeptides and nucleic acids encoding same Patent: WO 0136538-A 3 25-MAY-2001; PAT linear 7526 TTCCGGCTAAACCAGAGAACAACTGGCTTCCGGCGTTTT 7564 341 PheArgileAsnArgLysThrileGlyPhe***HisPhe 353 DNA Sequence 3 from Patent W00136638. AXI49447 Curagen Corporation (US) Location/Qualifiers GI:14347929 Homo sapiens (human) 1. .2011 Homo sapiens AX149447.1 7289 281 321 7229 6812 6872 6359 7109 221 7169 241 261 301 121 141 201 101 161 181 DEFINITION ORGANISM REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE RESULT 15 JOURNAL AX149447 LOCUS FEATURES g g 셤 엄 g g g g ò à δ à ò ò g ð à d ð d ð à à 8

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                                                                                                                                                                                                                                                                                                         1369 AACTGTGAGCCGGAGCAGCTGCCCATTGACCGCTGCTTACAGGACAATGGGCAGTGCCAT 1428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GluAlaAlaThrMetAlaThrTyrAsnGlnLeuSerTyr***GlnLysAlaLysTyrHis 100
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/db_xref="taxon:9606"
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